



FT PROPEP 22 76 OR 135 (POTENTIAL).  
 FT CHAIN 77 366 LEFT-RIGHT DETERMINATION FACTOR B.  
 FT DISULFID 251 264 BY SIMILARITY.  
 FT DISULFID 263 316 BY SIMILARITY.  
 FT DISULFID 293 351 BY SIMILARITY.  
 FT DISULFID 297 353 BY SIMILARITY.  
 FT CARBOHYD 158 158 N-LINKED (GLCNAC, . .) (POTENTIAL).  
 SEQUENCE 366 AA: 158 MW: BCF900C7IED9RAA CRC64;

Query Match 77.0%; Score 67; DB 1; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00023; PRT: 366 AA.  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGALVPRRLQ 13  
 b 353 CASDGALVPRRLQ 365

RESULT 2  
 ID TGFb\_HUMAN STANDARD;  
 AC 00292; 075611;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Endometrial bleeding-associated factor) (Left-right determination factor A)  
 DE (Lefty-A protein).  
 GN EBFA OR TGFb4 OR LEFTYA OR LEFTYA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97298127; PubMed=9153275;  
 RA "Detection of ebaf, a novel human gene of the transforming growth factor beta superfamily association of gene expression with endometrial bleeding";  
 RT J. Clin. Invest. 99:2342-2350(1997).  
 [2]  
 RN [2]  
 RP REVISIONS.  
 RX MEDLINE=99162193; PubMed=10053005;  
 RA Kothapalli R.;  
 RL Unpublished results, cited by:  
 RL Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,  
 RL Casey B.;  
 RL Am. J. Hum. Genet. 64:712-721(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT L-R AXIS MALFORMATIONS ASN-342.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99162193; PubMed=10053005;  
 RA Kosaki K., Bassi M.T., Kosaki R., Lewin M., Belmont J., Schauer G.,  
 RA Casey B.;  
 RT "Characterization and mutation analysis of human LEFTY A and LEFTY B, homologues of murine genes implicated in left-right axis development.";  
 RT Am. J. Hum. Genet. 64:712-721(1999).  
 CC -1 FUNCTION: REQUIRED FOR LEFT-RIGHT ASYMMETRY DETERMINATION OF ORGAN SYSTEMS IN MAMMALS. MAY PLAY A ROLE IN ENDOMETRIAL BLEEDING.  
 CC -1 SUBCELLULAR LOCATION: Secreted.  
 CC -1 TISSUE SPECIFICITY: MESENCHYMAL CELLS OF THE ENDOMETRIAL STROMA.  
 CC -1 DEVELOPMENTAL STAGE: TRANSIENTLY EXPRESSED BEFORE AND DURING MENSTRUAL BLEEDING.  
 CC -1 PTM: THE PROCESSING OF THE PROTEIN MAY ALSO OCCUR AT THE SECOND R- SITE LOCATED AT AA 132-135. PROCESSING APPEARS TO BE REGULATED IN A CELL-TYPE SPECIFIC MANNER.  
 CC -1 DISEASE: DEFECTS IN EBFA RESULT IN LEFT-RIGHT AXIS MALFORMATIONS INCLUDING LEFT PULMONARY ISOMERISM, CARDIAC ANOMALIES CHARACTERIZED BY COMPLETE ATRIOVENTRICULAR CANAL DEFECT AND

CC HYPOPLASTIC LEFT VENTRICLE, AND INTERRUPTED INFERIOR VENA CAVA.  
 CC !- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC DR U81523; AAC532699.1; ALT\_SEQ.  
 CC DR EMBL; AF081511; ANC32600.1;  
 CC DR EMBL; AF081508; AAC32600.1; JOINED.  
 CC DR EMBL; AF081509; AAC32600.1; JOINED.  
 CC DR EMBL; AF081510; ANC32600.1; JOINED.  
 CC DR EMBL; AF081513; AAD48145.1;  
 CC DR HSSP; P10560; 1TGJ.  
 CC DR MM; 601877;  
 CC DR InterPro; IPR001839; TGF-beta.  
 CC DR InterPro; IPR001111; TGFb\_N.  
 CC DR Pfam; PF00019; TGF-beta\_2.  
 CC DR Pfam; PF00688; TGFb\_Dpropeptide\_1.  
 CC DR ProDom; PD000357; TGF-beta\_1.  
 CC DR SMART; SM00204; TGFb\_1.  
 CC DR PROSITE; PS00250; TGF-BETA\_1.  
 CC KW Developmental protein; Growth factor; Cytokine; Glycoprotein; Signal; Multigene family; Disease mutation; POTENTIAL.  
 CC FT SIGNAL 1 21 BY SIMILARITY.  
 CC FT PROPEP 22 76 BY SIMILARITY.  
 CC FT CHAIN 77 366 BY SIMILARITY.  
 CC FT DISULFID 251 264 BY SIMILARITY.  
 CC FT DISULFID 263 316 BY SIMILARITY.  
 CC FT DISULFID 293 353 BY SIMILARITY.  
 CC FT DISULFID 297 353 BY SIMILARITY.  
 CC FT CARBOYD 158 158 S -> N (IN L-R AXIS MALFORMATIONS).  
 CC FT VARIANT 342 342 S -> N (IN L-R AXIS MALFORMATIONS).  
 CC SQ SEQUENCE 366 AA; 40920 MW; 63AA16CAE30F7A39 CRC64;  
 CC Query Match 77.0%; Score 67; DB 1; Length 366;  
 CC Best Local Similarity 100.0%; Pred. No. 0.00023;  
 CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGALVPRRLQ 13  
 DB 353 CASDGALVPRRLQ 365

RESULT 3  
 ID TGF4\_MOUSE STANDARD;  
 AC 064280;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-Oct-2001 (Rel. 40, Last annotation update)  
 DE Transforming growth factor beta 4 precursor (TGF-beta 4) (Lefty protein) (Lefty-1 protein) (STR43 protein).  
 GN EBFA OR TGFb4 OR STR43 OR LEFTY OR LEFTY1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1] NCBI\_TAXID=10090;  
 RN [1] TISSUE=Placenta;  
 RN MEDLINE=96202359; PubMed=8610011;  
 RX Memo C., Saijoh Y., Fujii H., Ikeda M., Yokoyama T., Yokoyama M.,  
 RA Toyota Y., Hamada H.;  
 RT "Left-right asymmetric expression of the TGF beta-family member Lefty in mouse embryos.";  
 RT Nature 381:151-155(1996).  
 RL RN [2]



[1] SEQUENCE FROM N.A.  
 RN RP SEQUENCE FROM N.A.  
 RA Yang W., Bai Q., Skrypka I., Zhao G., Somerville R.L.;  
 OC "The 5'-upstream regions of the trp operons of *Escherichia coli* and  
 Escherichia." NCBI\_TAXID=562;  
 OX [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN\_K12 / MG155;  
 RX MEDLINE=9726617; Pubmed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 MAU B., Shao Y., "The complete genome sequence of *Escherichia coli* K-12.",  
 "Science 277:1453-1474 (1997)."  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN\_K12; PubMed=9097039;  
 RX MEDLINE=97251357; Pubmed=9097039;  
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 Kasai H., Kashimoto K., Klimura S., Kitakawa M., Kitagawa M.,  
 Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motonura K.,  
 Nakade S., Nakamoto Y., Nashimoto H., Nishio Y., Oshima T., Saito M.,  
 Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,  
 Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;  
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL Res 3:363-377(1996).  
 CC -!- SIMILARITY: BELONGS TO THE TRPH FAMILY.  
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 DR AE000224; AAC74348.1;  
 EMBL; D90764; BAA14800.1; -;  
 DR EcoGene; EG14257; BAA14815.1; -;  
 DR InterPro; IPR004013; PHP\_C.  
 DR InterPro; IPR003141; PHP\_N.  
 DR Pfam; PF02811; PHP\_C; 1.  
 DR Pfam; PF02231; PHP\_N; 1.  
 DR SMART; SM00481; POLITIAC; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 293 AA; 32396 MW; BBDAFC33743B4FF4 CRC64;

[1] RESULT 7  
 TRPH\_HAEIN STANDARD; PRT; 274 AA.  
 ID TRPH\_HAEIN STANDARD; PRT; 274 AA.  
 AC P44176;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein TRPH.  
 GN TRPH OR H1400.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OX NCBI\_TAXID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN\_KD / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 McKenney K., Sutton G., FitzHugh W., Fields C.A., Gocayne J.D.,  
 Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 Weidman J.F., Phillips C.A., Spriggs T., Hedbom E., Cotton M.D.,  
 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

[1] RESULT 6  
 TRPH\_SALTY STANDARD; PRT; 293 AA.  
 ID TRPH\_SALTY STANDARD; PRT; 293 AA.  
 AC 054453;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Protein trph.  
 GN TRPH OR STM1721.  
 OS *Salmonella typhimurium*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC *Salmonella*.  
 OX NCBI\_TAXID=602;

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA "whole-genome random sequencing and assembly of Haemophilus  
 RT influenzae Rd.";  
 RL Science 269:496-511(1995).  
 CC -I- SIMILARITY: BELONGS TO THE TRPH FAMILY.

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CC EMBL; U32820; AAC23046.1; -.

DR TIGR; HI1400; -.

DR InterPro; IPR004013; PHP\_C.

DR InterPro; IPR00111; PHP\_N.

DR Pfam; PF02811; RHP\_C; 1.

DR Pfam; PF02231; PHP\_N; 1.

DR SMART; SM00481; POLIITAC; 1.

DR Complete proteome.

RW Sequence 274 AA; 30116 MW; F7ED7B0BDFB850D3 CRC64;

SQ

RESULT 8

HYPB\_RHOCA

ID HYPB\_RHOCA

AC P26410;

DT 01-AUG-1992 (Rel. 23, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Hydrogenase nickel incorporation protein hypB

OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).

OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;

NCBI\_TAXID=1067;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33303 / B10;

RX MEDLINE=93268050; PubMed=8497190;

RA Delbeau A., Richard P., Toussaint B., Caballero F.J., Elster C.,

RA Delphin C., Smith R.L., Chabert J., Vignais P.M.;

RT "Organization of the genes necessary for hydrogenase expression in

RT Rhodobacter capsulatus. Sequence analysis and identification of two

RT hyp regulatory mutants." Mol. Microbiol. 8:15-29 (1993).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91177833; PubMed=2007559;

RA Xu H.W., Wall J.D.;

RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter

RT capsulatus." Mol. Microbiol. 17:2401-2405(1991).

RL CC -I- FUNCTION: COULD BE INVOLVED IN NICKEL BINDING AND ACCUMULATION.

CC -I- SIMILARITY: BELONGS TO THE HYB/RHPM FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X61007; CAA13326.1; -;

DR EMBL; M5509; AAA72926.1; -;

DR D38532; D38532.

DR PIR; S21903; S21903.

DR InterPro; IPR02894; HYPB\_DreG.

DR Pfam; PF01495; HYPB\_UreI.

DR SMART; SM00481; RHPM\_N.

DR CHLDGAMYEQALAHLP; CHLDGAMYEQALAHLP.

DR Rfam.

DR Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

OX NCBI\_TAXID=340;

OX NCBI\_SEQUENCE FROM N.A.

RC SPRAIN-B100;

RX MEDLINE=94045213; PubMed=853667;

RA Kepplin R., Wang G., Hoette B., Priefer U.B., Puehler A.;

RT "A 3'-9-kb DNA region of Xanthomonas campestris pv. campestris that is

RT necessary for lipopolysaccharide production encodes a set of enzymes

RT involved in the synthesis of dtDP-rhamnose." J. Bacteriol. 175:7786-7792(1993).

RN [2]

RP REVISIONS TO 8 AND 15.

RA Vorholter F.J., Niehaus K., Puehler A.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

CC -I- CATALYTIC ACTIVITY: dtDP-glucose = dtDP-4-dehydro-6-deoxy-D-

CC glucose + H(2)O.

CC -I- COFACTOR: NAD.

CC -I- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN

CC BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.

CC -I- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE

CC DEHYDRATASE SUBFAMILY.

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CC DR EMBL; AF204145; AAK52466.1; -.

CC DR P27830; IBKX.

CC DR InterPro; IPR001509; Epimerase.

CC DR Pfam; PF01370; Epimerase; 1.

CC KW Lipopolysaccharide biosynthesis; Lyase; NAD.

CC PT NP\_BIND 8 14 NAD (POTENTIAL).

CC SQ SEQUENCE 351 AA; 38558 MW; F1B393B1R2EA0F3F CRC64;

Query Match 46.6%; Score 40.5; DB 1; Length 351;  
 Best Local Similarity 71.4%; Pred. No. 10;  
 Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 4 DGALYVPRRLQ-HRP 16  
 | | | | | | | | | |  
 Db 61 DGALYVTRLQQHQ 74

RESULT 10  
 OPS1\_PATE ID OPS1\_PATE STANDARD; PRT; 499 AA.  
 AC O1573; DT 15-JUL-1998 (Rel. 36, Created)  
 YP T 15-JUL-1998 (Rel. 36, Last sequence update)  
 T 30-MAY-2000 (Rel. 39, Last annotation update)  
 UE SCOP1.  
 OS patinopecten yesoensis (Ezo giant scallop) (Yesso scallop).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pectinoidae; Pectinidae; Patinopecten.  
 OX NCBI\_TAXID=6573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-EYE;  
 RX MEDLINE=97435252; PubMed=9287291;  
 RA Kojima D., Terakita A., Ishikawa T., Tsukahara Y., Maeda A.,  
 RA Shichida Y.;  
 RT "A novel Go-mediated phototransduction cascade in scallop visual  
 cells.";  
 RT J. Biol. Chem. 272:22979-22989 (1997).  
 CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT  
 CC MEDIATE VISION. THEY CONSIST OF AN APOTROPEIN, OPSIN, COVALENTLY  
 CC LINKED TO CIS-RETINAL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: RETINA. EXPRESSED IN THE DEPOLARIZING CELL  
 CC LAYER OF THE PHOTORECEPTOR CELLS DISTANT FROM THE LENS.  
 CC -!- BE PHOSPHORYLATED (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC OPSIN SUBFAMILY.

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 C or send an email to license@isb-sib.ch).

DR EMBL: AB006454; BA022217; -  
 DR InterPro; IPR00276; GPR\_Rhodpsn.  
 DR InterPro; IPR001760; Opsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PRO0237; GICRRHODOPSN.  
 DR PROSITE; PS00337; G-PROTEIN\_RECEP\_FL1; 1.  
 DR PROSITE; PS00338; G-PROTEIN\_RECEP\_FL2; 1.  
 DR PROSITE; PS00339; OPSIN; 1.  
 KW Phosphorylation; Retinal protein; Transmembrane; Glycoprotein; Vision;  
 KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.  
 FT DOMAIN 1 50 EXTRACELLULAR.  
 FT TRANSMEM 51 75 1 (POTENTIAL).  
 FT DOMAIN 76 87 CYTOPLASMIC.  
 FT TRANSMEM 88 114 2 (POTENTIAL).  
 FT DOMAIN 115 128 EXTRACELLULAR.  
 FT TRANSMEM 129 148 3 (POTENTIAL).  
 FT DOMAIN 149 168 CYTOPLASMIC.  
 FT TRANSMEM 169 192 4 (POTENTIAL).  
 FT DOMAIN 193 216 EXTRACELLULAR.  
 FT TRANSMEM 217 244 5 (POTENTIAL).  
 FT DOMAIN 245 278 CYTOPLASMIC.  
 FT TRANSMEM 279 302 6 (POTENTIAL).  
 FT DOMAIN 303 310 EXTRACELLULAR.  
 FT TRANSMEM 311 335 7 (POTENTIAL).  
 FT DOMAIN 336 499 CYTOPLASMIC.  
 FT DISULFID 125 203 BY SIMILARITY.  
 FT BINDING 322 322 RETINAL CHROMOPHORE.  
 FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 19 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 353 PALMITATE (BY SIMILARITY);  
 FT LIPID 354 PALMITATE (BY SIMILARITY);  
 SQ SEQUENCE 499 AA; 55945 MW; 853DIB7E3509EEA CRC64;

Query Match 46.0%; Score 40; DB 1; Length 499;  
 Best Local Similarity 66.7%; Pred. No. 18;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 VPRRLQHRP 16  
 Db 463 IPRVQHRP 471

RESULT 11  
 SPA1\_SYN3 ID SPA1\_SYN3 STANDARD; PRT; 695 AA.  
 AC P74576; DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Probable arginine decarboxylase 1 (EC 4.1.1.19) (ADC).  
 GN SPEA1 OR SPEA OR SLR062.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_TAXID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hiyama M., Sugiyama M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Ohumura S.,  
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.;  
 RL DNA Res. 3:109-136(1996).  
 CC -!- CATALYTIC ACTIVITY: L-arginine + CO(2).  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (By similarity).  
 CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM  
 CC ARGinine.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine  
 CC DECARBOXYLASES.  
 CC -!- DECARBOXYLASES.  
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 CC -!- DECARBOXYLASES.  
 DR EMBL: D90916; BA18683; 1; -  
 DR InterPro; IPR00183; Orn\_DAP\_Arg\_decarboxylase.  
 DR Pfam: PF02784; Orn\_Arg\_dec\_N\_1  
 DR Pfam: PF00278; Orn\_DAP\_Arg\_dec\_C\_2.  
 DR PRINTS; PRO1179; ODAORBXASE\_2.  
 DR PROSITE; PS00878; ODR\_DC\_2-1.  
 DR PROSITE; PS00879; ODR\_DC\_2-2; 1.  
 KW Spermidine biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate;  
 KW Complete Proteome.  
 FT DOMAIN 332 342 SUBSTRATE-BINDING (POTENTIAL).  
 SQ SEQUENCE 695 AA; 78238 MW; E90EB699D66320D CRC64;

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Query Match Score 40; DB 1; Length 695;  
Best Local Similarity 72.7%; Pred. No. 26;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 6 ALVPRRLQHQP 16  
  |: 111111 |  
Db 208 ALLARRLCHRP 218

RESULT 12  
NIRB\_ECOLI STANDARD PRT; 847 AA.

ID NIRB\_ECOLI STANDARD PRT; 847 AA.  
AC P08205;  
DT 01-AUG-1995 (Rel. 08, Created)  
  |: 32 |  
  |: 01-NOV-1995 (Rel. 32, Last sequence update)  
  |: 32 |  
  |: 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nitrite reductase [NAD(P)H] large subunit (EC 1.6.6.4).  
GN NIRB OR B3365.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
  |: 1 |  
CC Escherichia.  
CX NCBI\_TaxID=562;  
RN [1]  
FP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RA MEDLINE=89282391; PubMed=2543955;  
RA Bell A.I., Gaston K.L., Cole J.A., Busby S.J.W.;  
RA "Cloning of binding sequences for the Escherichia coli transcription  
activators, FNR and CRP: location of bases involved in discrimination  
between FNR and CRP";  
RA Nucleic Acids Res. 17:3865-3874(1989).  
RN [2]  
FP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RA MEDLINE=90345936; PubMed=2200672;  
RA Peakman T., Crouzet J., Mayaux J.F., Busby S.J.W., Mohan S.,  
RA Harbone N., Wootten J., Nicolson R., Cole J.A.;  
RA "Nucleotide sequence, organisation and structural analysis of the  
products of genes in the nirB-cysG region of the Escherichia coli  
K-12 Chromosome";  
RA Eur. J. Biochem. 191:315-323(1990).  
RN [3]  
FP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mathew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RA "The complete genome sequence of Escherichia coli K-12";  
RA Science 277:1433-1474(1997).  
RN [4]  
FP SEQUENCE OF 1-21; FROM N.A.  
RX MEDLINE=88062713; PubMed=2445993;  
RA Jayaraman P.S., Peakman T.C., Busby S.J.W., Quincey R.V.,  
RA Cole J.A.;  
RA "Location and sequence of the promoter of the gene for the NADH-  
dependent nitrite reductase of Escherichia coli and its regulation by  
oxygen, the Fnr protein and nitrate";  
RA J. Mol. Biol. 196:781-788(1987).  
CC -I- CATALYTIC ACTIVITY: 3 NAD(P)(+ ) + NH(4)OH +  
  |: H(2)O.  
CC -I- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS  
  |: A SIROHEME AND ONE 2PE-2S IRON-SULFUR CENTER.  
CC -I- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENTRIFICATION).  
CC -I- SUBUNIT: HOMODIMER WHICH ASSOCIATES WITH NIRD.  
CC -I- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN  
  |: FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND  
  |: SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).  
CC -I- This SWISS-PROT entry is copyright. It is produced through a collaboration  
  |: between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC -I- EMBL; AE000412; AAC76390.1; -.  
DR PIR; S00529; S00529.  
DR PIR; S10791; S10791.  
DR Ecodene; EG10653; nirB.  
DR InterPro; IPR01322; FAD PYR\_redox.  
DR InterPro; IPR000660; Nir\_Sir.  
DR Pfam; PF01077; Nir\_Sir; 1.  
DR Pfam; PF00070; PYR\_redox; 1.  
DR PRINTS; PRO0397; STROHAEM.  
DR PROSITE; PS000365; NIR\_SIR; 1.  
KW Oxidoreductase; FAD; Flavoprotein; Iron-sulfur; Nitrate assimilation;  
  |: Heme; NADP; Complete proteome.  
KW FAD (POTENTIAL).  
FT NP\_BIND 44 79  
FT NP\_BIND 193 225  
FT METAL 641 641  
FT METAL 647 647  
FT METAL 681 681  
FT METAL 685 685  
FT CONFLICT 442 442  
FT CONFLICT 835 847  
SQ SEQUENCE B47 AA: 93121 MW: 5265AD93FD390EB4 CRC4;  
  |: 1 |  
Query Match Score 46.08; Score 40; DB 1; Length 847;  
Best Local Similarity 70.0%; Pred. No. 32; Mismatches 1; Indels 2; Gaps 0;  
Matches 7; Conservative 1; Gaps 0;  
  |: 1 |  
Qy 7 LYPRRLQHQP 16  
  |: 1 |  
Db 822 MYPEREQHRP 831  
  |: 1 |  
RESULT 13  
NOS3\_BOVIN STANDARD PRT; 1204 AA.  
ID NOS3\_BOVIN  
AC P2473;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type  
III) (NOSIII) (Endothelial NOS) (ENOS) (Constitutive NOS) (CNOS).  
DE NOS3.  
GN Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92335295; PubMed=1378626;  
RA Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;  
RA "Endothelial nitric oxide synthase: molecular cloning and  
characterization of a distinct constitutive enzyme isoform.";  
RA Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93055452; PubMed=1385480;  
RA Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P.,  
RA Uematsu M., Neren R.M., Alexander R.W., Murphy T.J.;  
RA "Molecular cloning and characterization of the constitutive bovine  
aortic endothelial cell nitric oxide synthase.";  
RL J. Clin. Invest. 90:2092-2096(1992).  
RN [3]

SEQUENCE FROM N.A.  
TISSUE:Aortic endothelium;  
MEDLINE=92348367; PubMed=1379225;

RA Sessa W.C., Harrington J.K., Barbour C.M., Zeng D., Durieux M.E.,  
RA D'Angelo D.D., Lynch K.R., Peach M.J.;  
RT "Molecular cloning and expression of a cDNA encoding endothelial cell  
nitric oxide synthase.";  
RL J. Biol. Chem. 267:15274-15276(1992).  
RN [4]

RP MYRISTOYLATION.  
RX MEDLINE=93231982; PubMed=7682550;

RA Busconi L., Michel T.;  
RT "Endothelial nitric oxide synthase. N-terminal myristoylation  
determines subcellular localization.",  
RL J. Biol. Chem. 268:8410-8413(1993).  
RN [5]

RP PALMITOYLATION.  
RX MEDLINE=96102197; PubMed=8524847;

RA Rabin L.I., Michel T.;  
RT "Mutagenesis of palmitoylation sites in endothelial nitric oxide  
synthase identifies a novel motif for dual acylation and subcellular  
targeting.",  
RL J. Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).  
RN [6]

P X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.  
RX MEDLINE=99091052; PubMed=975848;

RA Raman C.S., Li H., Martasek P., Kral V., Masters B.S., Poulos T.L.;  
RT "Crystal structure of constitutive endothelial nitric oxide synthase:  
a paradigm for pterin function involving a novel metal center.",  
RL Cell 95:939-950(1998).  
RN [7]

RP X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS) OF 66-481.  
RX MEDLINE=20503854; PubMed=1101558;

RA Li H., Raman C.S., Martasek P., Kral V., Masters B.S., Poulos T.L.;  
RT "Mapping the active site polarity in structures of endothelial  
nitric oxide synthase heme domain complexed with isothioureas.";  
RL J. Inorg. Biochem. 81:133-139(2000).  
RN [8]

RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
RX MEDLINE=21229525; PubMed=11331003;

RA Raman C.S., Li H., Martasek P., Masters B.S.S., Poulos T.L.;  
RT "Crystallographic studies on endothelial nitric oxide synthase  
complexed with nitric oxide and mechanism-based inhibitors.",  
RL Biochemistry 40:5399-5406(2001).  
RN [9]

RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
RX MEDLINE=2152923; PubMed=1169589;

RA Raman C.S., Li H., Martasek P., Southan G., Masters B.S.S.,  
RA Poulos T.L.;  
RT "Crystal structure of nitric oxide synthase bound to nitro indazole  
reveals a novel inactivation mechanism.",  
RL Biochemistry 40:13448-13455(2001).  
RN [10]

P X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).  
RX MEDLINE=21336567; PubMed=11331280;

RA Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,  
RA Masters B.S.S., Poulos T.L.;  
RT "Implications for isoform-selective inhibitor design derived from the  
binding mode of bulky isothioureas to the heme domain of endothelial  
nitric oxide synthase.";  
RL J. Biol. Chem. 276:26486-26491(2001).

-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN  
VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL  
TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH  
FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND  
PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETERS.

CC -I- CATALYTIC ACTIVITY: L-Lysine + N NADPH + M O(2) = Citrulline +  
nitric oxide + N NADP(+).

CC -I- COFACTOR: Heme. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES  
TERAHYDROBIOCPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF  
THE ENZYME.

CC -I- ENZYME REGULATION: STIMULATED BY CALMODULIN/CALMODULIN.

CC -I- SUBUNIT: HOMODIMER.

-!- SIMILARITY: BELONGS TO THE NOS FAMILY.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; M90057; AAA30667; 1; -;  
CC DR EMBL; M89952; AAA30494; 1; -;  
CC DR EMBL; M93674; AAA30669; 1; -;  
CC DR PDB; 1NSE; 1B-MAY-99.  
CC DR PDB; 2NSE; 25-MAY-99.  
CC DR PDB; 3NSE; 1B-MAY-99.  
CC DR PDB; 4NSE; 1B-MAY-99.  
CC DR PDB; 8NSE; 21-NOV-01.  
CC DR PDB; 9NSE; 25-OCT-00.  
CC DR PDB; 1DIW; 25-OCT-00.  
CC DR PDB; 1ED4; 25-OCT-00.  
CC DR PDB; 1DM6; 13-DEC-00.  
CC DR PDB; 1DM7; 13-DEC-00.  
CC DR PDB; 1DM8; 13-DEC-00.  
CC DR PDB; 1DM1; 20-DEC-00.  
CC DR PDB; 1DMJ; 20-DEC-00.  
CC DR PDB; 1ED5; 31-JAN-01.  
CC DR PDB; 1ED6; 31-JAN-01.  
CC DR PDB; 1FO1; 20-JUL-01.  
CC DR PDB; 1FOL; 20-JUL-01.  
CC DR PDB; 1FOO; 20-JUL-01.  
CC DR PDB; 1FOP; 20-JUL-01.  
CC DR PDB; 1FQ1; 16-NOV-01.  
CC DR InterPro; IPR003097; FAD binding.  
CC DR PDB; 1D1X; 25-JUL-01.  
CC DR PDB; 1D1Y; 25-JUL-01.  
CC DR PDB; 1D0C; 21-NOV-01.  
CC DR PDB; 1D0O; 21-NOV-01.  
CC DR InterPro; IPR001433; Oxidored-FAD.  
CC DR Pfam; PF00667; FAD binding; 1.  
CC DR InterPro; IPR001094; Flavodoxin-like.  
CC DR InterPro; IPR001226; Flavodoxin.  
CC DR InterPro; IPR001709; Flavopyrid\_cyt\_redctse.  
CC DR PRINTS; PR004030; NOS.  
CC DR PRINTS; PR00339; FLAVODOXIN.  
CC DR PROSITE; PS60001; NOS; 1.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;  
KW Lipoprotein; Palmitate; Phosphorylation; Calcium-binding; Heme;  
KW Zinc; Metal-binding; Multigene family; 3D-structure.  
FT INIT\_MET 0  
FT BINDING 185  
FT DOMAIN 491 511  
FT NP\_BIND 650 681  
FT NP\_BIND 794 805  
FT NP\_BIND 936 946  
FT NP\_BIND 1011 1029  
FT NP\_BIND 1109 1124  
FT LIPID 1 1  
FT LIPID 14 14  
FT LIPID 25 25  
FT METAL 95 95  
FT METAL 100 100  
FT MOD\_RES 142 142  
FT CONFLICT 99 99  
FT CONFLICT 164 164  
FT CONFLICT 317 327  
FT CONFLICT 454 454  
FT CONFLICT 458 458



RE MEDLINE=98012228; PubMed=9348312;

RA Kuo F.C., Sklar J.L.;

RA "Augmented expression of a human gene for 8-oxoguanine DNA glycosylase  
RT (MuEM) in B lymphocytes of the dark zone in lymph node germinal  
RT centers";

RT J. Exp. Med. 186:1547-1556(1997).

RL RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 1A);

RX SEQUENCE FROM N.A. (ISOFORM 1A);

RA MEDLINE=98026507; PubMed=9321410;

RA Bjorras M., Luna L., Johansen B.E., Hoff E., Haug T., Rognes T.,  
Seeberg E.;

RA "Opposite base-dependent reactions of a human base excision repair  
RT enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites.";

RT [9]

RN RP SEQUENCE FROM N.A. (ISOFORM 1A);

RA Dhennaut A., Boiteux S., Radicella J.;

RT "Genomic structure and promoter characterization of the human 8-OH-  
guanine glycosylase gene (OGG1) gene.,"

RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RL RN [10]

RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

RX MEDLINE=99380087; PubMed=10449904;

RA Ishida T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,  
A A Nishiura S., Aburatani H.;

RT "Structure and chromosome location of human OGG1.";

RT Cytoogenet. Cell Genet. 85:232-236(1999).

RL RN [11]

RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

RX MEDLINE=99250167; PubMed=10233168;

RA Nishiura K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,  
RA Nakabeppu Y.;

RT "Expression and differential intracellular localization of two major  
RT forms of human 8-Oxoguanine DNA glycosylase encoded by alternatively  
RT spliced OGG1 mRNAs.";

RT Mol. Biol. Cell 10:1637-1652(1999).

RL RN [12]

RP REVIEW.

RX MEDLINE=202395648; PubMed=10775435;

RA Boiteux S., Radicella J.P.;

RT "The human OGG1 gene: structure, functions, and its implication in the  
RT process of carcinogenesis.";

RT Arch. Biochem. Biophys. 377:1-8(2000).

RL RN [13]

RP VARIANT HIS-154.

RX MEDLINE=96438755; PubMed=9765518;

RA Shimamura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J.;

RT "In frequent mutations of the OGG1 gene, that is involved in the  
RT excision of 8-hydroxyguanine in damaged DNA, in human gastric  
RT cancer.";

RT Jpn. J. Cancer Res. 89:825-828(1998).

RL RN [14]

RP VARIANT GLN-46.

RX MEDLINE=93324718; PubMed=9662341;

RA Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F.,  
Dherin C., Radicella J. P., Dizdaroglu M., Boiteux S.;

RA "Oudart S., Dutrillaux B., Boiteux S.;"

RT "Mutations in OGG1, a gene involved in the repair of oxidative DNA  
RT damage, are found in human lung and kidney tumours.";

RT Oncogene 16:3083-3086(1998).

RL RN [15]

RP CHARACTERIZATION OF VARIANT CYS-326.

RX MEDLINE=94286532; PubMed=10497264;

RA Dherin C., Radicella J. P., Dizdaroglu M., Boiteux S.;

RA "Excision of oxidatively damaged DNA bases by the human alpha-hOGG1  
RT protein and the polymorphic alpha-hOGG1(Ser326Cys) protein which is  
RT frequently found in human populations.";

RT Nucleic Acids Res. 27:4001-4007(1999).

RL RN [16]

RP CHARACTERIZATION OF VARIANTS GLN-46; HIS-154 AND CYS-326.

RX MEDLINE=20368636; PubMed=10908322;

RA Audibert M., Radicella J.P., Dizdaroglu M.;

RT "Effect of single mutations in the OGG1 gene found in human tumors on  
RT the substrate specificity of the ogg1 protein.";

Fri Sep 10 11:24:49 2002

us-09-674-254-3.rsp

Page 11

Search completed: September 10, 2002, 10:46:42  
Job time: 120 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 10, 2002, 10:43:37 ; Search time 15.15 Seconds  
(without alignments)  
101.480 Million cell updates/sec

Title: US-09-674-254-3  
Perfect score: 87  
Sequence: 1 CASDGALYPRRLQHQP 16

scoring table: BLOSUM62

Gapop 10.0 , Gapextb=0.5

searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_711:

1: Pirl1\*

2: Pir2;\*

3: Pir3;\*

4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	75.9	368	2 S67507	morphogen lefty precursor - mouse
2	45	51.7	293	2 E04874	C:Species: Mus musculus (house mouse)
3	45	51.7	293	2 F90858	C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
4	45	51.7	293	2 A85761	C:Accession: S67507
5	44	50.6	293	2 A06653	R:Neno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, T.; Toyoda, Y.; Nature 381, 151-155, 1996.
6	44	50.6	522	2 D81900	A:Title: Left-right asymmetric expression of the TGF-beta-family member lefty in mouse
7	44	50.6	522	2 A81124	A:Reference number: S67507;
8	43	49.4	274	2 F64027	A:Molecule type: mRNA
9	42.5	48.9	656	2 S55262	A:Cross-references: EXBL:D83921; NID:91325920; PID:BA12121.1; PID:d1012795; PID:g14
10	42	48.3	335	2 D38532	A:Note: the authors translated the codon ACG for residue 241 as His
11	41.5	47.7	327	1 S72913	C:Keywords: growth factor
12	41	47.1	606	2 AD1219	F:78-368/Product: morphogen lefty #status predicted <MAT1>
13	41	47.1	606	2 AG1572	F:136-368/Product: morphogen lefty #status predicted <MAT2>
14	40.5	46.6	351	2 B49906	Query Match 75.9%; Score 66; DB 2; Length 368;
15	40	46.0	106	2 H75553	Best Local Similarity 92.3%; Pred. No. 0.00077; Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
16	40	46.0	289	2 H75553	RESULT 1 CASDGALYPRRLQ 13
17	40	46.0	335	2 F84411	:
18	40	46.0	695	2 S76771	Db 355 CASDGALYPRRLQ 367
19	40	46.0	847	2 H91155	RESULT 2
20	40	46.0	847	2 H65130	Probable metal-dependent phosphoesterase Yciv - Escherichia coli
21	40	46.0	847	2 E86001	C:Species: Escherichia coli
22	40	46.0	1205	1 A38943	C:Accession: E64874
23	39.5	45.4	262	2 E98265	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Rose, D.J.; Mau, B.; Shao, Y.
24	39.5	45.4	262	2 AD3019	Science 277, 1453-1462, 1997
25	39	44.8	109	2 T49452	A:Title: The complete genome sequence of Escherichia coli K-12.
26	39	44.8	248	2 S73168	A:Reference number: A64720; MJD:9426617
27	39	44.8	346	2 T45069	A:Accession: E64874
28	39	44.8	545	2 A87448	A:Status: nucleic acid sequence not shown; translation not shown
29	39	44.8	682	2 T28899	A:Molecule type: DNA
					A:Residues: 1-293 <MAT1>
					A:Cross-references: GB:AB00224; GB:U00096; NID:91787509; PID: AAC74348.1; PID:g17875
					A:Experimental source: strain K-12, substrate MG1655
					C:Genetics:
					A:Gene: yciv
					C:Superfamily: hypothetical protein HI1400
					Query Match 51.7%; Score 45; DB 2; Length 293;

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Best Local Similarity 64.3%; Pred. No. 3.3%; Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
2Y 2 ASDGALVPRLQRH 15
Db 18 ASPGCCLPPEALVHR 31

RESULT 3
F90858 probable enzymes [Imported] - Escherichia coli (strain O157:H7, substrate RIMD 0509952)
;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
;Accession: F90858
;Author: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Yokoyama, K.; Han, C.G.; Jasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
;Reference number: A99629; MUID:21156231; PMID:11258796
;Accession: F90858
;Status: preliminary
;Molecule type: DNA
;Residues: 1-293 <HAY>
;Cross-references: GB:BA000007; PIDN:BAB35261.1; PID:913361303; GSPPDB:GN00154
;Experimental source: strain O157:H7, substrate RIMD 0509952
;Genetics:
;Gene: Ecs1838
;Superfamily: hypothetical protein HI1400

Query Match 51.7%; Score 45; DB 2; Length 293;
Best Local Similarity 64.3%; Pred. No. 3.3%; Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
2Y 2 ASDGALVPRLQRH 15
Db 18 ASPGCCLPPEALVHR 31

RESULT 4
I85761 probable enzymes yciV yciV [Imported] - Escherichia coli (strain O157:H7, substrate EDU9
;Species: Escherichia coli
;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
;Accession: A85761
;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassner, J.D.; Ross, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lin, A.; Dimaranta, E.; Potanousis, K.; Apodaca, Nature 409, 529-533, 2001
;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
;Reference number: A85480; MUID:21074935; PMID:11206551
;Accession: A85761
;Status: preliminary
;Molecule type: DNA
;Residues: 1-293 <STO>
;Cross-references: GB:AE005174; NID:912515531; PIDN:AAG56549.1; GSPPDB:GN00145; UMGPP:Z25
;Experimental source: strain O157:H7, substrate ED1933
;Genetics:
;Gene: yciV
;Superfamily: hypothetical protein HI1400

Query Match 51.7%; Score 45; DB 2; Length 293;
Best Local Similarity 64.3%; Pred. No. 3.3%; Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
2Y 2 ASDGALVPRLQRH 15
Db 18 ASPGCCLPPEALVHR 31

RESULT 5
I60653 conserved hypothetical protein STR1329 [Imported] - Salmonella enterica subsp. enterica

```

A; Reference number: A81000; MUID:20175755  
A; Accession: A81124  
A; Status: Preliminary  
A; Molecule type: DNA  
A; Residues: 1-522 <TET>  
A; Cross-references: GB:AE002459; GB:AE002098; NID:97226320; PIDN:AAF41487.1; PID:g722633  
A; Experimental source: serogroup B, strain MC58  
C; Genetics:  
A; Gene: NMB1095  
C; Superfamily: Haemophilus influenzae hypothetical protein HI1501

Query Match 50.6%; Score 44; DB 2; Length 522;  
Best Local Similarity 57.1%; Pred. No. 8.9;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Y 3 SGDALVPRRLQHPR 16  
Db 143 SGDGLVPRNFIRHP 156

RESULT 8  
F61027 hypothetical protein HI1400 - Haemophilus influenzae (strain Rd KW20)  
C;Species: Haemophilus influenzae  
C;Accession: F64027  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, N.S.M.  
Science 269, 496-512, 1995  
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A;Reference number: A64000; MUID:95350630  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A; Residues: 1-274 <TIGR>  
A; Cross-references: GB:U32820; GB:L42023; NID:91574231; PIDN:AC23046.1; PID:g1574235; T  
C; Superfamily: hypothetical protein HI1400

Query Match 49.4%; Score 43; DB 2; Length 274;  
Best Local Similarity 64.3%; Pred. No. 7;  
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLQHR 15  
Db 13 ASDGVSPTELYHR 26

RESULT 9  
S55262 5'v-endonuclease - Neurospora crassa  
C;Species: Neurospora crassa  
C;Accession: S55262  
R;Yajima, H.; Takao, M.; Yasuhira, S.; Zhao, J.H.; Ishii, C.; Inoue, H.; Yasui, A.  
EMBO J. 14, 2391-2399, 1995  
A;Title: A eukaryotic gene encoding an endonuclease that specifically repairs DNA damage  
A;Reference number: S55262; MUID:95392980  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A; Residues: 1-56 <TAJ>  
A; Cross-references: EMBL:D11392; NID:g1526560; PID:g927215  
C; Genetics:  
A; Gene: uvel

Query Match 48.9%; Score 42.5; DB 2; Length 656;  
Best Local Similarity 64.3%; Pred. No. 21;  
Matches 9; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CASD---GALVPRRLQHPR 16  
Db 119 CFSELVAGAIVLRRQYRP 137

Query Match 47.7%; Score 41.5; DB 1; Length 327;  
Best Local Similarity 52.6%; Pred. No. 15;  
Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 CASD---GALVPRRLQHPR 16  
Db 119 CFSELVAGAIVLRRQYRP 137

RESULT 12									
Query Match 46.6%; Score 40.5; DB 2; Length 351;									
Best Local Similarity 71.4%; Pred. No. 25;									
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: ADI219									
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker-Huet, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.									
Science 294: 849-852, 2001									
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, H.									
A;Title: Comparative genomics of <i>Listeria</i> species									
A;Reference number: AB1077; MUID:21537279; PMID:11679669									
A;Accession: ADI219									
R; Status: Preliminary									
Molecule type: DNA									
Residues: 1-606 <GLA>									
Cross references: GB:NC_003210; PIDN:CAC99234_1; PID:916410572; GSPDB:GN00177									
Experimental source: strain EGD-e									
Genetics:									
Gene: lm01156									
Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain									
RESULT 15									
Query Match 46.6%; Score 40.5; DB 2; Length 351;									
Best Local Similarity 71.4%; Pred. No. 25;									
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: ADI219									
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker-Huet, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.									
Science 294: 849-852, 2001									
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, H.									
A;Title: Comparative genomics of <i>Listeria</i> species									
A;Reference number: AB1077; MUID:21537279; PMID:11679669									
A;Accession: ADI219									
R; Status: Preliminary									
Molecule type: DNA									
Residues: 1-606 <GLA>									
Cross references: GB:NC_003210; PIDN:CAC99234_1; PID:916410572; GSPDB:GN00177									
Experimental source: strain EGD-e									
Genetics:									
Gene: lm01156									
Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain									
RESULT 16									
Query Match 46.6%; Score 40.5; DB 2; Length 351;									
Best Local Similarity 71.4%; Pred. No. 25;									
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
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R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: ADI219									
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker-Huet, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.									
Science 294: 849-852, 2001									
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, H.									
A;Title: Comparative genomics of <i>Listeria</i> species									
A;Reference number: AB1077; MUID:21537279; PMID:11679669									
A;Accession: ADI219									
R; Status: Preliminary									
Molecule type: DNA									
Residues: 1-606 <GLA>									
Cross references: GB:NC_003210; PIDN:CAC99234_1; PID:916410572; GSPDB:GN00177									
Experimental source: strain EGD-e									
Genetics:									
Gene: lm01156									
Superfamily: Klebsiella oxytoca diol dehydratase-reactivating factor large chain									
RESULT 17									
Query Match 46.6%; Score 40.5; DB 2; Length 351;									
Best Local Similarity 71.4%; Pred. No. 25;									
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: B49066									
R; Koeplin, R.; Wang, G.; Priefer, U.B.; Puehler, A.									
J. Bacteriol. 151: 7786-7792, 1993									
A;Title: A 3.9-kb DNA region of <i>Xanthomonas campestris</i> pv. <i>campestris</i> that is necessary for virulence									
A;Reference number: A9906; MUID:94075213									
A;Accession: ADI219									
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker-Huet, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.									
Science 294: 849-852, 2001									
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno,									

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GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 10, 2002, 10:40:47 ; Search time 30.11 Seconds
          (without alignments)
          59.023 Million cell updates/sec

Title: US-09-674-254-3
Perfect score: 87
Sequence: 1 CASIDGALVPRRLQHRP 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 74754 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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9:	2	87	100.0	294	'22 AAB3940	TGF beta 4 amino a
10:	3	87	100.0	370	'21 AAY92013	Human transforming
11:	4	67	77.0	120	'20 AAW93160	Human Lefty-2 prot
12:	5	67	77.0	120	'20 AAW93159	Human Lefty-1 prot
13:	6	67	77.0	366	'20 AAY172870	Human bone morphog
14:	7	67	77.0	366	'20 AAY11871	Human bone morphog
15:	8	67	77.0	366	'20 AAY13363	Amino acid sequenc
16:	9	67	77.0	366	'20 AAY038850	Human lefly protei
17:	10	67	77.0	366	'20 AAY0287	EGF-like homologue
18:	11	67	77.0	366	'21 AAY088575	Human PRO317 amino

## ALIGNMENTS

RESULT	1		
AAY5026			
ID	AAY5026	standard; peptide; 16 AA.	
XX			
AC	AAY5026;		
XX			
DT	18-FEB-2000	(first entry)	
XX			
Human ebaF protein antigenic C-terminal peptide.			
Antigenic; ebaF; human; fertility; diagnosis; endometrial irregularity;			
endometrial bleeding-associated factor; contraceptive; endometrium;			
fertility-regulating; uterine bleeding; non-receptiveness; marker;			
infertility; conception; in vitro fertilization; artificial insemination			
XX			
OS			Homo sapiens.
XX			

W09555902-A1  
04-NOV-1999.  
29-APR-1999;  
29-APR-1998;  
(UYSF-) UNIV  
Tabibzadeh S;  
WWPI; 2000-052  
Diagnosis of  
variants, par-

סודות

result No.	Score	% Query Match			DB	ID	Description
		Length	DB	ID			
1	87	100.0	16	'21	AAY10826		Human eba9 protein
2	87	100.0	294	22	AAB35940		TGF-Beta 4 amino
3	87	100.0	370	21	AAV92013		Human Transformin
4	67	77.0	120	20	AAW93160		Human Lefty-2 pro
5	67	77.0	120	20	AAW93159		Human Lefty-1 pro
6	67	77.0	366	20	AAV17870		Human bone morpho
7	67	77.0	366	20	AAV17871		Human bone morpho
8	67	77.0	366	20	AAY113363		Amino acid sequen
9	67	77.0	366	20	AAV03850		Human Lefty prote
10	67	77.0	366	20	AAV05287		EGF-like homologu
11	67	77.0	366	21	AAV88575		Human PRO117 amino

S Claim 39; Page 95; 112pp; English.

CX This invention describes a novel method for diagnosing endometrial irregularities by screening an endometrial sample, or body fluid, for the presence of ebaf (endometrial bleeding-associated factor) or its splice variants that are differentially expressed. The product of the invention has contraceptive and fertility-regulating activity. Ebaf is associated with natural or abnormal uterine bleeding and is a marker for non-receptiveness of the endometrium, and is aberrantly expressed in a subset of infertile women. The method is used for diagnosis, monitoring and prognosis of infertility, endometriosis and abnormal uterine bleeding, particularly to determine endometrial receptivity (i.e. for optimizing the time of conception, including by in vitro fertilization and artificial insemination methods). Ebaf is also useful as a contraceptive while agents that down regulate it, e.g. antisense sequences, are used to treat endometrial disorders, specifically to restore fertility. This sequence represents an antigenic peptide derived from the human ebaf protein C-terminal.

Q Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 7e-09; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CASDGALVPRLQHRP 16  
| | | | | | | | | | | |  
D 1 casdgalvprlqhrp 16

RESULT 2

D AAB35940 standard; protein; 294 AA.

X AAB35940;

X 26-FEB-2001 (first entry)

X TGF-beta 4 amino acid sequence.

X Heparin binding; vascular graft; matrix; cell adhesion; growth factor; wound healing; dermal wound; wound healing; TGF-beta 4.  
X Unidentified.

N WO2000064481-A1.

D 02-NOV-2000.

X 22-APR-1999; 99WO-IB00800.

P 22-APR-1999; 99WO-IB00800.

A (ETHZ-) ETH ZURICH & UNIV ZURICH.

I Sakiyama SE, Hubbell JA;

R WPI; 2001-024627/03.

X Matrix for controlled release of growth factor for wound healing, has substrate that attaches heparin binding peptide (HBP), a peptide comprising a binding domain which binds heparin with high affinity, heparin or heparin-like polymer, and a protein growth factor or peptide fragment which has a domain that binds heparin with low affinity.

S Example 5; Page 21; 48pp; English.

X This invention relates to a matrix comprising a substrate capable of comprising a binding domain which binds heparin with high affinity, heparin or heparin-like polymer, and a protein growth factor or peptide fragment which has a domain that binds heparin with low affinity. Included in the invention is a vascular graft comprising the matrix,

which is capable of supporting cell adhesion. The matrix is used for delivering low heparin binding affinity growth factor proteins or peptides in a controlled manner suitable for wound healing. The matrix can be used in an article for treating dermal wounds, and in an implantable sterilized composition capable of supporting cell adhesion. The present sequence represents a growth factor protein. The protein is used in an example illustrating that non-heparin-binding growth factors can be released in a controlled manner from heparin-based drug delivery systems based on their low affinity for heparin.

Sequence 294 AA;

Query Match 100.0%; Score 87; DB 22; Length 294;

Best Local Similarity 100.0%; Pred. No. 1.5e-07; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGALVPRLQHRP 16  
| | | | | | | | | | | |  
Db 275 casdgalvprlqhrp 290

RESULT 3

AAY92013 standard; Protein: 370 AA.

XX AAY92013;

AC XX

DT 19-JUL-2000 (first entry)

XX DE Human transforming growth factor beta 4/ebaft monomer.  
XX KW human transforming growth factor beta 4 monomer; ebaft; CKSF; mutant; cystine knot growth factor; hairpin loop; infertility.  
XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 1..266  
FT /Label= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor."  
FT FT

FT FT /note= "mutant optionally comprises one or more substitutions in these residues."  
FT FT

FT FT /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor."  
FT FT

FT FT /note= "mutant optionally comprises one or more substitutions in these residues."  
FT FT

FT FT /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor."  
FT FT

FT FT /note= "mutant optionally comprises one or more substitutions in these residues."  
FT FT

FT FT /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor."  
FT FT

FT FT /note= "mutant optionally comprises one or more substitutions in these residues."  
FT FT

FT FT /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor."  
FT FT

OS WO200017360-A1.

XX 30-MAR-2000.

XX 19-MAR-1999;

XX 22-SEP-1998;

XX 98WO-US19772.

PA (UWY-M) UNIV MARYLAND BALTIMORE.

PI Weintraub BD, Szkludlinski MW;

XX DR WPI; 2000-283585/24.

OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
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 NAME/KEY: Domain  
 LOCATION: 97..98  
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 LOCATION: 116..117  
 OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
 FEATURE:  
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 LOCATION: 282..283  
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 FEATURE:  
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 LOCATION: 872..873  
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 FEATURE:  
 NAME/KEY: Domain  
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 OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
 FEATURE:  
 NAME/KEY: Domain  
 LOCATION: 114..116  
 OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
 FEATURE:  
 NAME/KEY: Domain  
 LOCATION: 1202..1203  
 OTHER INFORMATION: /note= "Potential proline directed phosphorylation site"  
 FEATURE:  
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 LOCATION: 1411..1413  
 OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
 FEATURE:

NAME/KEY: Domain  
 LOCATION: 168..170  
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 LOCATION: 633..635  
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 NAME/KEY: Domain  
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 NAME/KEY: Domain  
 LOCATION: 1051..1053  
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 FEATURE:  
 NAME/KEY: Domain  
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 OTHER INFORMATION: /note= "cAMP dependent phosphorylation site"  
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 Qy 1 CASDGALVPRRLQHRP 16  
 Db 100 CCLGSLVLPRKLQTRP 115  
 RESULT 4  
 US-09-428-517-3  
 Sequence 3, Application US/09428517  
 Patent No. 6251636  
 GENERAL INFORMATION:  
 APPLICANT: Betlach, Mary C.  
 APPLICANT: Shah, Sanjay Krishnakant  
 APPLICANT: McDaniel, Robert  
 APPLICANT: Tang, Li  
 TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE  
 FILE REFERENCE: 30062-20029.00  
 CURRENT APPLICATION NUMBER: US/09/428,517  
 CURRENT FILING DATE: 1999-10-28  
 EARLIER APPLICATION NUMBER: 60/120,254  
 EARLIER FILING DATE: 1999-02-16  
 EARLIER APPLICATION NUMBER: 60/106,100  
 EARLIER FILING DATE: 1998-10-29  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 3816  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Recombinant Oleandolide PKs  
 OTHER INFORMATION: US-09-428-517-3  
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 Best Local Similarity 45.0%; Pred. No. 4, 4e+02;  
 Matches 3; Mismatches 3; Indels 5; Gaps 1;  
 Qy 2 ASDGALVPR----RLQHRP 16  
 Db 3586 AADGTLPPLSGLIVVRHRP 3605

RESULT 5  
US-09-067-782A-5  
Sequence 5 Application US/09067782A  
Patent No. 6165751

GENERAL INFORMATION:  
APPLICANT: BARNES, MICHAEL  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rainer & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,782A  
FILING DATE: 28-APR-1998

SEQUENCE CHARACTERISTICS:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: UK 9710734.6  
FILING DATE: 23-MAY-1997  
APPLICATION NUMBER: EP 97309144.0  
FILING DATE: 13-NOV-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 601-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-067-782A-2

RESULT 7  
US-09-171-461-32  
Sequence 32 Application US/09171461  
Patent No. 6335016

GENERAL INFORMATION:  
APPLICANT: Baker, Adam  
APPLICANT: Cotter, Matthew  
APPLICANT: Chiocca, Susanna  
APPLICANT: Kurzbauer, Robert  
APPLICANT: Schaffner, Gotthold  
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus  
FILE REFERENCE: 06521800000  
CURRENT APPLICATION NUMBER: US/09/171,461  
CURRENT FILING DATE: 199-01-12  
EARLIER APPLICATION NUMBER: PCT/EP97/01944  
EARLIER FILING DATE: 1997-04-18  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 439  
TYPE: PRT  
ORGANISM: CELO VIRUS  
FEATURE:  
OTHER INFORMATION: Position: 5366..6685/Product:IVa2  
US-09-171-461-32

RESULT 6  
US-09-067-782A-2  
Sequence 2 Application US/09067782A  
Patent No. 6165751

GENERAL INFORMATION:  
APPLICANT: BARNES, MICHAEL  
TITLE OF INVENTION: NOVEL COMPOUNDS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rainer & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980

COMPUTER READABLE FORM:

Qy 1 CASDGALVPRRLQHGP 16  
|| : : ||

Db 206 CREDGTIAPKTSTFRP 221

RESULT 8  
 US-09-300-909-21  
 Sequence 21, Application US/09300909  
 Patent No. 6306580  
 GENERAL INFORMATION:  
 APPLICANT: PREPARATION OF HUMAN PAPILLOMAVIRUS E1 HAVING  
 TITLE OF INVENTION: HELICASE ACTIVITY AND METHOD THEREFOR  
 NUMBER OF SEQUENCES: 27  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/300,909  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/083,942  
 FILING DATE: 01-MAY-1998  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 506 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-300-909-21

Query Match 43.7% Score 38; DB 4; Length 506;  
 Best Local Similarity 53.3%; Pred. No. 58;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 2 ASDGALVPRRLQHP 16  
 Db 396 ALDGNLVSMDVKHP 410

RESULT 9  
 US-08-472-666-3  
 Sequence 3, Application US/08472666  
 Patent No. 5821048  
 GENERAL INFORMATION:  
 APPLICANT: Howley, Peter M.  
 APPLICANT: Benson, John D.  
 APPLICANT: Yasugi, Toshiharu  
 APPLICANT: Sakai, Hiroyuki  
 TITLE OF INVENTION: METHOD AND KIT FOR DIAGNOSING  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ann Louise Kerner, Ph.D.  
 STREET: 200 State Street  
 CITY: Boston  
 STATE: MA  
 COUNTY: USA  
 ZIP: 01209

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kerner, Ann Louise  
 REGISTRATION NUMBER: 33,523  
 REFERENCE/DOCKET NUMBER: HAZ-010PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-330-1300  
 TELEFAX: 617-330-1311  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 649 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Human papillomavirus-16 E1  
 STRAIN: HPV-16  
 PCT-US96-07615-3

REGISTRATION NUMBER: 33,194  
 REFERENCE/DOCKET NUMBER: HAZ-010  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-330-1300  
 TELEFAX: 617-330-1311  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 649 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Human papillomavirus-16 E1  
 STRAIN: HPV-16  
 US-08-472-666-3

Query Match 43.7% Score 38; DB 5; Length 649;  
 Best Local Similarity 53.3%; Pred. No. 76;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Query Match 43.7% Score 38; DB 5; Length 649;  
 Best Local Similarity 53.3%; Pred. No. 76;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ASDGALVPRRLOHRRP 16 ; EARTIER APPLICATION NUMBER: US-08/553,503  
 US-08-319-866-10 ; EARLIER FILING DATE: 1996-03-01  
 Db 539 ALDGNEVSMYDKHRP 553 ; EARLIER APPLICATION NUMBER: P4411402.8  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 1205  
 ; TYPE: PRT  
 ; ORGANISM: Cytomegalovirus  
 US-09-123-708-6

RESULT 11 ;  
 US-08-319-866-10 ; Sequence 10, Application US/08319866  
 ; Patent No. 529223 ; GENERAL INFORMATION:  
 ; APPLICANT: Regulski, Michael  
 ; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/319,866  
 FILING DATE: 7-OCT-1994  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granahan, Patricia  
 REGISTRATION NUMBER: 32,227  
 REFERENCE/DOCKET NUMBER: CSHL94-03  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (617) 861-6240  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1205 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-319-866-10

Query Match 43.1%; Score 37.5%; DB 2; Length 1205;  
 best Local Similarity 69.2%; Pred. No. 1.9e+02;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 5 GALV-PRRLOHRRP 16 ; EARTIER APPLICATION NUMBER: US-08/553,503  
 US-09-123-708-6 ; Sequence 6, Application US/09123708  
 ; Patent No. 6146887 ; GENERAL INFORMATION:  
 ; APPLICANT: SCHRADER, Juergen  
 ; APPLICANT: GOEDEKE, Axel  
 ; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
 ; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
 ; FILE REFERENCE: 511169-2004  
 ; CURRENT APPLICATION NUMBER: US/09/123,624  
 ; CURRENT FILING DATE: 1998-07-28  
 ; PRIORITY NUMBER: 08/553,503  
 ; PRIOR FILING DATE: 1996-03-01  
 ; PRIORITY NUMBER: 4411402.8  
 ; PRIOR FILING DATE: 1994-03-31  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 6  
 ; LENGTH: 1205  
 ; TYPE: PRT  
 ; ORGANISM: Bos taurus  
 US-09-123-624-6

Query Match 43.1%; Score 37.5%; DB 4; Length 1205;  
 best Local Similarity 69.2%; Pred. No. 1.9e+02;  
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 5 GALV-PRRLOHRRP 16 ; EARTIER APPLICATION NUMBER: US-08/553,503  
 US-08-858-207A-373 ; Sequence 373, Application US/08858207A  
 ; Patent No. 6348328 ; GENERAL INFORMATION:  
 ; APPLICANT: Black, Michael  
 ; APPLICANT: Hodgeson, John  
 ; APPLICANT: Knowles, David  
 ; APPLICANT: Nicholas, Richard  
 ; APPLICANT: Stoddola, Robert  
 ; TITLE OF INVENTION: No. 6348328el Compounds  
 ; NUMBER OF SEQUENCES: 552  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA

RESULT 12 ;  
 US-09-123-708-6 ; Sequence 6, Application US/09123708  
 ; Patent No. 6146887 ; GENERAL INFORMATION:  
 ; APPLICANT: SCHRADER, Juergen  
 ; APPLICANT: GOEDEKE, Axel  
 ; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
 ; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
 ; FILE REFERENCE: 511169-2003  
 ; CURRENT APPLICATION NUMBER: US/09/123,708  
 ; CURRENT FILING DATE: 1998-07-28

COUNTRY: USA  
 ZIP: 19406-0939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FasCSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/858-207A  
 FILING DATE: 09-MAY-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/017670  
 APPLICATION NUMBER: 60/017670  
 FILING DATE: 14-MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gianni, Edward R  
 REGISTRATION NUMBER: 38-891  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: P50475  
 TELEPHONE: 610-270-4478  
 TELEFAX: 610-270-5050  
 TELELEX:  
 INFORMATION FOR SEQ ID NO: 373:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 137 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 6348328E  
 US-08-858-207A-373

Query Match 42.5%; Score 37; DB 4; Length 137;  
 Best Local Similarity 66.7%; Pred. No. 21;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LYPRRLQHR 15  
 Db 2 LVPKRVKHR 10

RESULT 15  
 US-08-414-926A-26  
 Sequence 26, Application US/08414926A  
 GENERAL INFORMATION:  
 APPLICANT: Spaete, Richard  
 APPLICANT: Cha, Tai-an  
 TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 STREET: 5 Palo Alto Square  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306-2155  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/414,926A  
 FILING DATE: March 31, 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Csair, Luann  
 REGISTRATION NUMBER: 31,822  
 REFERENCE/DOCKET NUMBER: AVIR-011/OOUS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-494-7622  
 TELEFAX: 415-857-0663

---

INFORMATION FOR SEQ-ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 336 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 IMMEDIATE SOURCE:  
 CLONE: tol.22  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..336  
 OTHER INFORMATION: /label= UL151  
 US-08-414-926A-26

Query Match 42.5%; Score 37; DB 1; Length 336;  
 Best Local Similarity 46.7%; Pred. No. 56;  
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 CASDGALVPRRLOHR 15  
 Db 213 CSQHGAFFPARHLHR 227

Search completed: September 10, 2002, 10:45:32  
 Job time: 165 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 10:42:47 ; Search time 12.84 Seconds  
(without alignments)  
30.437 Million cell updates/sec

Title: US-09-674-254-3  
Perfect score: 87  
Sequence: 1 CASDGALVPRRLQHRP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:  
1: /cgnd2\_6/ptodata/2/1aa/5A..COMB.pep:  
2: /cgnd2\_6/ptodata/2/1aa/5B..COMB.pep:  
3: /cgnd2\_6/ptodata/2/1aa/6A..COMB.pep:  
4: /cgnd2\_6/ptodata/2/1aa/6B..COMB.pep:  
5: /cgnd2\_6/ptodata/2/1aa/PCTUS..COMB.pep:  
6: /cgnd2\_6/ptodata/2/1aa/backfile1..pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description	
1	67	77.0	366	3	US-09-987-304A-2	Sequence 2, Appli	
2	67	77.0	366	3	US-09-987-304A-4	Sequence 4, Appli	
3	40	46.0	1205	1	US-07-908-245-2	Sequence 3, Appli	
4	38.5	44.3	3816	4	US-09-428-517-3	Sequence 5, Appli	
5	5	38	43.7	121	4	US-09-067-782A-5	Sequence 2, Appli
6	58	43.7	1251	4	US-09-067-782A-2	Sequence 32, Appli	
7	38	43.7	439	4	US-09-171-611-32	Sequence 21, Appli	
8	38	43.7	506	4	US-09-300-909-21	Sequence 3, Appli	
9	38	43.7	649	5	US-08-472-666-3	Sequence 3, Appli	
10	38	43.7	649	5	PCT-US96-07615-3	Sequence 10, Appli	
11	37.5	43.1	1205	2	US-08-319-666-10	Sequence 6, Appli	
12	37.5	43.1	1205	2	US-09-123-708-4	Sequence 6, Appli	
13	37.5	43.1	1205	4	US-09-123-624-6	Sequence 6, Appli	
14	37	42.5	137	4	US-08-858-207A-373	Sequence 373, Appli	
15	37	42.5	336	1	US-08-414-926A-26	Sequence 26, Appli	
16	37	42.5	336	2	US-08-926-522-26	Sequence 26, Appli	
17	37	42.5	336	3	US-09-253-882-26	Sequence 26, Appli	
18	37	42.5	325	4	US-09-527-657-26	Sequence 6, Appli	
19	37	42.5	395	3	US-08-981-125-6	Sequence 6, Appli	
20	37	42.5	395	4	US-09-480-784-6	Sequence 6, Appli	
21	36	41.4	95	4	US-09-142-078-62	Sequence 62, Appli	
22	36	41.4	95	4	US-09-357-141-62	Sequence 62, Appli	
23	36	41.4	924	2	US-08-588-983-18	Sequence 18, Appli	
24	36	41.4	924	2	US-08-588-976-18	Sequence 18, Appli	
25	36	41.4	2476	2	US-08-276-667-2	Sequence 2, Appli	
26	35	40.2	20	2	US-08-934-015-120	Sequence 120, Appli	
27	35	40.2	255	4	US-09-355-166-3	Sequence 3, Appli	

## ALIGNMENTS

RESULT 1  
US-08-987-304A-2  
; Sequence 2, Application US/08987904A  
; Patent No. 6027917  
; GENERAL INFORMATION:  
; APPLICANT: Celeste, Anthony J.  
; APPLICANT: Murray, Beth  
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN (BMP)- 17 AND BMP-18  
; NUMBER OF SEQUENCES: 7  
; COMPOSITIONS:  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/987, 904A  
; FILING DATE: 10-DEC-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAYAR, STEVEN R  
; REGISTRATION NUMBER: 32,618  
; REFERENCE/DOCKET NUMBER: GI 5307  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8769  
; TELEFAX: (617) 876-8581  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-987-904A-2

Query Match Score 67; DB 3; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.00024;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CASDGLVPRRLQ 13  
Db 353 CASDGLVPRRLQ 365

RESULT 2  
US-08-987-904A-4  
Sequence 4, Application US/08987904A  
; Patent No. 6027917  
; GENERAL INFORMATION:  
; APPLICANT: Celeste, Anthony J.  
; APPLICANT: Murray, Beth  
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN (BMP) - 17 AND BMP-18  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 7  
; COMPOSITIONS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/987, 904A  
; FILING DATE: 10-DEC-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LAZAR, STEVEN R.  
; REGISTRATION NUMBER: 32, 618  
; REFERENCE/DOCKET NUMBER: GI 5307  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8769  
; TELEFAX: (617) 876-8501  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 366 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-987-904A-4

Query	1	CASDGALVPRRLQ	13
Match	77.0%	Score 67;	DB 3;
Local	100.0%	Pred. No. 0.00024;	Length 366;
Similarity		Mismatches 0;	Indels 0
Matches	13;	Conservative	

SULT, 3  
-07-908-245-2  
; Sequence 2, Application US/07908245  
; Patent No. 5498539  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, David G.  
; APPLICANT: Alexander, R. Wayne  
; APPLICANT: Murphy, T.J.  
; APPLICANT: Nishida, Ken'ichi  
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kilpatrick, Cody  
; STREET: 1100 Peachtree St. NW  
; CITY: Atlanta  
; STATE: GA  
; ZIP: 30309  
; COUNTRY: USA

SEARCHED: 140 Peachtree Street, Suite 2800  
INDEXED:  
FILED:  
SERIALIZED:  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

FEATURE: NAME/KEY: Domain  
LOCATION: 53 - 54  
OTHER INFORMATION: /note- "Potential proline directed phosphorylation site"  
FEATURE: NAME/KEY: Domains  
LOCATION: 58 - 59

PT New mutant cystine knot growth factor proteins comprising one or more  
 PT mutant subunits, useful for treating or preventing diseases e.g.  
 PT hypothyroidism and thyroid cancer

XX Claim 238; Page 302; 320pp; English.

XX This is the wild type human transforming growth factor beta 4 monomer.

CC Mutants comprise at least one electrostatic charge altering mutation in a  
 CC beta hairpin loop, resulting in increased bioactivity.

CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more  
 CC mutant subunits and having novel properties or improved pharmacological  
 CC properties, compared to wild type CKGFs, are claimed. The CKGF  
 CC superfamily comprises at least four families of growth factors: the  
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,  
 CC the neurotrophins and the transforming growth factor-beta family; the  
 CC families are known to be structurally similar (especially comprising the  
 CC cystine knot topology), and it was shown that mutations at certain  
 CC positions in the CKGF hairpin loops of family members and other members  
 CC of the CKGF superfamily could significantly alter the biological  
 CC activities of the CKGF.

CC Mutant transforming growth factor family proteins or analogues are useful  
 CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained  
 CC infertility, time-limited conception and in assisted reproduction.

XX Sequence 370 AA;

Query Match 100.0%; Score 87; DB 21; Length 370;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGALVPRQLQHPRP 16  
 Db 351 casdgalvprqlqhp 366

RESULT 4  
 AAW93160 standard; Protein; 120 AA.

XX AAW93160;  
 AC WO9906444-A1.  
 XX DT 21-MAY-1999 (first entry)  
 XX DE Human Lefty-2 protein fragment.

DE Lefty-2; human; growth differentiation factor; detection: ovarian; colon;  
 KW treatment; cell proliferative disorder; immunological disease;  
 KW muscle; musculodegenerative disorder; tissue repair; burn; contraceptive;  
 KW premature labour; fetal growth; cancer; gonadal; adrenal; tumour;  
 KW endometrial.  
 XX Homo sapiens.  
 XX WO9906443-A1.  
 XX PR 31-JUL-1997; 97US-0054381.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX PI Huynh TV, Lee S, Sebald S;  
 XX DR N-PSDB; AAX22359.  
 XX PF 24-JUL-1998; 98WO-US15174.  
 XX PR 31-JUL-1997; 97US-0054381.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX PI Huynh TV, Lee S, Sebald S;  
 XX DR N-PSDB; AAX22359.  
 XX PS Example 1; Figure 1; 38pp; English.

XX This sequence represents a novel human growth differentiation factor, Lefty-2. Molecules of the invention may be used to detect or treat cell  
 CC proliferative or immunological disorders, including disease processes  
 CC involving muscle such as musculodegenerative disorders or tissue repair following trauma or burns, in contraceptive regimens, to prevent  
 CC premature labour, to enhance fetal growth or development, or to treat  
 CC various cancers, including gonadal and adrenal tumours, endometrial and  
 CC ovarian tumours and colon cancer.

XX Sequence 120 AA;

XX AAW93159 standard; Protein; 120 AA.

XX AAW93159;  
 AC AAW93159;  
 XX DT 21-MAY-1999 (first entry)  
 XX DE Human Lefty-1 protein fragment.

XX KW Lefty-1; human; growth differentiation factor; detection: ovarian; colon;  
 KW treatment; cell proliferative disorder; immunological disease;  
 KW muscle; musculodegenerative disorder; tissue repair; burn; contraceptive;  
 KW premature labour; fetal growth; cancer; gonadal; adrenal; tumour;  
 KW endometrial.  
 XX Homo sapiens.  
 XX WO9906444-A1.  
 XX PR 11-FEB-1999.  
 XX PD 11-FEB-1999.  
 XX PF 24-JUL-1998; 98WO-US15352.  
 XX PR 31-JUL-1997; 97US-0054382.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX PI Huynh TV, Lee S, Sebald S;  
 XX DR N-PSDB; AAX22358.  
 XX PT A new growth differentiation factor, Lefty-1 - useful to detect and  
 PT treat cell proliferative and immunological disorders  
 XX Example 1; Figure 1; 38pp; English.

XX This sequence represents a novel human growth differentiation factor, Lefty-1. The polynucleotides, proteins and antibodies described in the  
 CC invention may be used to detect or treat cell proliferative or  
 CC immunological disorders, including disease processes involving muscle  
 CC such as musculodegenerative disorders or tissue repair following trauma  
 CC or burns, in contraceptive regimens, to prevent premature labour, to  
 CC enhance fetal growth or development, or to treat various cancers  
 CC including gonadal and adrenal tumours, endometrial and ovarian tumours,  
 CC and colon cancer.

XX Sequence 120 AA;

XX A new growth differentiation factor, Lefty-2 - useful to detect and  
 PT treat cell proliferative and immunological disorders  
 XX Example 1; Fig 1; 38pp; English.

Query Match 77.0%; Score 67; DB 20; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 0.00024;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 353 casdgalyprrlq 365  
 |||||||  
 1 CASDGALYPRRLQ 13  
 |||||||  
 Db 107 casdgalyprrlq 119  
 |||||

RESULT 7  
 AAY17871 standard; Protein; 366 AA.  
 XX  
 ID AAY17871  
 AC AAY17871;  
 AC AAY17871;  
 AC AAY17871;  
 DT 20-AUG-1999 (first entry)  
 DE Human bone morphogenic protein BMP-18.  
 KW Human; bone morphogenic protein; BMP-17; cartilage; tendon;  
 KW connective tissue defect; ligament; meniscus; wound healing; growth;  
 KW differentiation; epidermis; muscle; nerve; cardiac muscle.  
 DE Human bone morphogenic protein BMP-17.  
 KW Human; bone morphogenic protein; BMP-17; cartilage; tendon;  
 KW connective tissue defect; ligament; meniscus; wound healing; growth;  
 KW differentiation; epidermis; muscle; nerve; cardiac muscle.  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FT 1..142  
 FT /label= pro-peptide  
 FT 143..366  
 FT /label= BMP-17  
 PN W09929718-A2.  
 PD 17-JUN-1999.  
 PT 98WO-US24613.  
 PR 17-NOV-1998;  
 PR 10-DEC-1997;  
 PR 10-DEC-1997;  
 PR 97US-0987904.  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 New Purified bone morphogenic protein-17 and -18 (BMP-17 and BMP-18)  
 PT polypeptides, useful for the induction of growth and/or  
 PT differentiation of undifferentiated embryonic and stem cells  
 XX  
 Claim 20: Page 38-39; 39pp; English.  
 XX  
 The present sequence is a human bone morphogenic protein designated  
 BMP-18. BMP proteins are useful for the induction of growth and/or  
 differentiation of undifferentiated embryonic and stem cells, and for  
 the treatment of bone, cartilage and other connective tissue defects  
 including tendons, ligaments and meniscus, in wound healing and related  
 tissue repair, and for treatment of disorders and defects to tissues  
 which include epidermis, nerve, muscle, including cardiac muscle, and  
 other tissues and wounds, and organs such as liver, lung, epithelium,  
 brain, spleen, cardiac, pancreas and kidney tissue. DNA encoding BMP  
 proteins can be useful as probes to detect expression of BMP proteins,  
 and the vectors containing DNA encoding BMP proteins are useful for  
 delivery of the BMP proteins to cells of a patient.

XX  
 Sequence 366 AA;

Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 353 casdgalyprrlq 365  
 |||||||  
 1 CASDGALYPRRLQ 13  
 |||||

RESULT 8

AY13363		PR 24-NOV-1997; PR 24-NOV-1997;	97US-0066511.
ID AAY13363 standard; Protein; 366 AA.		XX PA (GETH ) GENENTECH INC.	
XX AC		XX PI	Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX DT 25-JUN-1999 (first entry)		XX DR	WPI: 1999-229533/19.
DE Amino acid sequence of protein PRO317.		XX DR N-PSDB; AAN52234.	New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
XX KW Secreted protein; transmembrane; human; enterocolitis;		XX PT	Claim 12; Fig 42; 320pp; English.
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;		XX PS	AY13344-403 represent secreted and transmembrane human proteins.
KW congenital microvillus atrophy; skin disease; cell growth;		XX CC	The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
KW abnormal keratinocyte; psoriasis; epithelial cancer;		CC CC	The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions
KW Parkinson's disease; Alzheimer's disease; AUS; neuropathy;		CC CC	(e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophyia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;		XX SQ	Sequence 366 AA;
XX anti-thrombotic; wound healing; tissue repair.		Query Match 77.0%; Score 67; DB 20; Length 366;	
OS Homo sapiens.		Best Local Similarity 100.0%; Pred. No. 0.00078;	
XX PF 16-SEP-1998; 98WO-US19330.		Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX PR 25-NOV-1997; 97US-0066840.		Qy 1 CASDGALVPRRLQ 13	
PR 25-MAR-1999.		Db 353 casdgalvprrlq 365	
XX PR 16-SEP-1998; 98WO-US19330.		RESULT 9	
XX PR 25-NOV-1997; 97US-0066840.		ID AAY03850 standard; Protein: 366 AA.	
PR 25-MAR-1999.		XX ID AAY03850	
XX PR 17-SEP-1997; 97US-0059113.		AC AAY03850;	
PR 17-SEP-1997; 97US-0059117.		DT 18-JUN-1999 (first entry)	
PR 17-SEP-1997; 97US-0059119.		XX DE Human lefty protein.	
PR 17-SEP-1997; 97US-0059121.		XX KW Nodal protein; lefty protein; TGF-beta; sexual development; human; pituitary; cartilage; osteoarthritis; osteoporosis; haematoepoiesis; periodontal disease; wound healing; tissue repair; tumour; cancer; interstitial lung disease; autoimmunity; leukaemia; lymphoma; immunity; immunosuppression; inflammatory bowel disease; myelosuppression; infectious disease; bone.	
PR 17-SEP-1997; 97US-0059184.		XX OS Homo sapiens.	
PR 18-SEP-1997; 97US-0059246.		XX FH Key	
PR 18-SEP-1997; 97US-0062125.		FT Peptide 1..18	
PR 15-OCT-1997; 97US-0062125.		FT Protein /note= "signal peptide"	
PR 17-OCT-1997; 97US-0062285.		FT FT 19..366 /note= "mature protein"	
PR 17-OCT-1997; 97US-0062287.			
PR 21-OCT-1997; 97US-0063486.			
PR 24-OCT-1997; 97US-0062814.			
PR 24-OCT-1997; 97US-0063045.			
PR 24-OCT-1997; 97US-0063120.			
PR 24-OCT-1997; 97US-0063121.			
PR 24-OCT-1997; 97US-0063127.			
PR 24-OCT-1997; 97US-0063128.			
PR 27-OCT-1997; 97US-0063329.			
PR 27-OCT-1997; 97US-0063337.			
PR 28-OCT-1997; 97US-0063541.			
PR 28-OCT-1997; 97US-0063542.			
PR 28-OCT-1997; 97US-0063554.			
PR 28-OCT-1997; 97US-0063550.			
PR 28-OCT-1997; 97US-0063556.			
PR 29-OCT-1997; 97US-0064345.			
PR 29-OCT-1997; 97US-0063704.			
PR 29-OCT-1997; 97US-0063732.			
PR 29-OCT-1997; 97US-0063738.			
PR 29-OCT-1997; 97US-0064215.			
PR 29-OCT-1997; 97US-0063735.			
PR 31-OCT-1997; 97US-00633870.			
PR 31-OCT-1997; 97US-0064103.			
PR 03-NOV-1997; 97US-0064248.			
PR 07-NOV-1997; 97US-0064809.			
PR 12-NOV-1997; 97US-0065185.			
PR 12-NOV-1997; 97US-0065846.			
PR 18-NOV-1997; 97US-0065693.			
PR 21-NOV-1997; 97US-0066120.			
PR 21-NOV-1997; 97US-0066364.			
PR 24-NOV-1997; 97US-0066772.			
PR 24-NOV-1997; 97US-0066466.			
PR 24-NOV-1997; 97US-0066770.			

Domain 78..364 Homo sapiens  
 FT /note= "first predicted TGF-beta like domain of lefty"  
 FT 136..366 OS  
 FT /note= "second predicted TGF-beta like domain of lefty"  
 FT 143..366 PN WO914327-A2.  
 FT /note= "third predicted TGF-beta like domain of lefty"  
 XX PD 25-MAR-1999.  
 PN WO909198-A1. XX PF 10-SEP-1998;  
 XX PD 25-FEB-1999. XX PR 25-NOV-1997;  
 XX PF 20-AUG-1998; 98WO-US17211. PR 17-SEP-1997;  
 XX PR 21-AUG-1997; 97US-0056565. PR 18-SEP-1997;  
 PA (HUMA) HUMAN GENOME SCI INC. PR 15-OCT-1997;  
 PA PT Ruben SM, Soppet DR; PR 17-OCT-1997;  
 XX DR; 1999-190173-16. PR 17-OCT-1997;  
 DR N-PSDB; AAX31925. PR 24-OCT-1997;  
 PT XX PR 29-OCT-1997; 97US-0056285.  
 XX PA (GENETH ) GENENTECH INC. PR 29-OCT-1997;  
 XX PI Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA;  
 PI Roy M, Wood WI; XX  
 PS DR WPI; 1999-220532/19.  
 PS DR N-PSDB; AAX28437.

(X) New isolate human Nodal and Lefty polypeptides  
 PT XX Antibodies against specific proteins overexpressed in tumours  
 XX Example 1; Fig 30; 130pp; English.  
 PS XX This sequence represents the EGF-like homologue EBAF-2.  
 PS XX The invention relates to antibodies (Ab) that bind to any of the  
 PS CC polypeptides (I) designated PRO187, PRO533, PRO214, PRO240, PRO211,  
 PS CC PRO30; PRO261; PRO246 or EBAF-2. The Ab, or other agents that inhibit  
 PS CC expression and/or activity of (I) are used: (i) to inhibit growth of  
 PS CC tumours; and (ii) as diagnostic/prognostic reagents for detection or  
 PS CC quantification of (I) in cells or tissues, by standard immunoassays, with  
 PS CC overexpression being indicative of cancer. For therapeutic use, the Ab  
 PS CC may be conjugated to a toxin, chemotherapeutic agent or radioisotope.  
 PS CC Genes expressing (I), many of which are growth factor homologues, are  
 PS CC overexpressed in some cases of cancer.  
 XX Sequence 366 AA;

Query Match 77.0%; Score 67; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078; Mismatches 0; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1  
 AAY88575 Standard; Protein: 366 AA.  
 XX AC AAY88575;  
 ID AAY88575 (first entry)  
 AC AAY88575;  
 XX DT 09-AUG-2000 (first entry)  
 ID Human PRO317 amino acid sequence.  
 AC AAY88575;  
 XX DE Human PRO317 amino acid sequence.  
 XX KW Antibody; PRO187; PRO533; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;  
 KW cell growth; proliferation; transforming growth factor; ADEPT;  
 KW antibody dependent enzyme mediated prodrug therapy.

RESULT 10  
 AAY05287 standard; Protein: 366 AA.  
 ID AAY05287  
 AC AAY05287;  
 XX DT 22-JUN-1999 (first entry)  
 XX DE EGF-like homologue EBAF-2.  
 XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;  
 KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;  
 KW FGF-8 homologue.  
 XX OS Homo sapiens.  
 PN WO200015666-A2.

XX 23-MAR-2000. PR 02-MAY-2000; 2000JP-0183767.  
 XX PR 09-JUN-2000; 2000JP-0241899.  
 PR 08-SEP-1999; 99WO-US20594.  
 XX (HELI-) HELIX RES INST.  
 PR 10-SEP-1998; 98US-0099803.  
 PR 10-SEP-1998; 98WO-US18824.  
 XX PA (GETH ) GENENTECH INC.  
 PR Goddard A, Gurney AL, Hillian KJ, Roy MA, Wood WI, Botstein D;  
 XX WPI: 2000-271386/23.  
 DR N-PSDB; AAA3056.  
 XX  
 New isolated antibodies which bind to specific polypeptides used for  
 diagnosis and treatment of neoplastic cell growth and proliferation -  
 PS Example 9; Fig 18; 200pp; English.  
 XX This sequence represents a human PRO317 amino acid sequence. PRO317  
 CC shares sequence homology with members of the transforming growth factor  
 beta superfamily of proteins. The invention relates to isolated  
 CC antibodies which bind to a polypeptide. The "PRO" polypeptides are  
 CC encoded by genes which are over expressed in the genome of tumour cells.  
 CC Vectors and host cells comprising the nucleic acid encoding the  
 CC antibodies are used in the production of the antibodies. The antibodies  
 CC and nucleic acids encoding them are used for diagnosing a tumour in a  
 CC mammal. The antibodies are used for inhibiting the growth of tumour cells  
 CC and identifying compounds that inhibit a biological or immunological  
 CC activity of and/or expression of a PRO187, PRO533, PRO214, PRO20,  
 CC PRO230, PRO261, PRO246 or PRO317 polypeptide. The antibody can be  
 CC used in antibody dependent enzyme mediated prodrug therapy (ADEPT) by  
 CC conjugating the antibody to a prodrug activating enzyme which converts a  
 CC prodrug to an anti-cancer drug. The antibodies can be fluorescently  
 CC labelled and monitored by light microscopy, flow cytometry or fluorimetry  
 CC for diagnosis and prognosis of tumours.  
 XX Sequence 366 AA;

Query Match 77.0%; Score 67; DB 21; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078; Length 366;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGALVPRRLQ 13  
 AC |||||||||  
 DB 353 casdgalvprrlq 365

RESULT 12  
 ID AAB95157 standard; Protein; 366 AA.  
 XX AC AAB95157;  
 XX DT 26-JUN-2001 (first entry)  
 XX DE Human protein sequence SEQ ID NO:17194.  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX OS Homo sapiens.  
 XX EP1074617-A2.  
 XX PD 07-FEB-2001.  
 XX PF 28-JUL-2000; 2000EP-0116126.  
 XX PR 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX PA (HELI-) HELIX RES INST.  
 XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX DR WPI: 2001-318749/34.  
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PR full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs .  
 XX DR WPI: 2001-318749/34.  
 XX PS Claim 8; SEQ ID 17194; 2537pp + CD ROM; English.  
 XX The present invention describes primer sets for synthesising 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesising polynucleotides  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAB03166 to AAB13628 and  
 CC AAB13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAB13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.  
 XX SQ Sequence 366 AA;

Query Match 77.0%; Score 67; DB 22; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078; Length 366;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASDGALVPRRLQ 13  
 AC |||||||||  
 DB 353 casdgalvprrlq 365

RESULT 13  
 ID AAB68600 standard; Protein; 366 AA.  
 XX ID AAB68600 standard; Protein; 366 AA.  
 XX AC AAB68600;  
 XX DT 27-APR-2001 (first entry)  
 XX DE PRO317.  
 XX KW Cytostatic; PRO protein; tumour; cancer.  
 XX OS Homo sapiens.  
 XX PN WO200105836-A1.  
 XX PD 25-JAN-2001.  
 XX PR 20-DEC-1999; 99WO-US30999.  
 PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.  
 PR 08-SEP-1999; 99WO-US20534.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21050.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 02-DEC-1999; 99WO-US28564.  
 XX PA (GETH ) GENENTECH INC.  
 PI Botstein D, Goddard A, Gurney AL, Hillian KJ, Roy MA, Wood WI;  
 XX WPI: 2001-091968/10.  
 DR N-PSDB; AA/F60376.  
 XX PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,  
 PT useful for diagnosing and treating cancers -  
 XX PS Claim 61: Fig 18; 196pp; English.  
 XX CC The present invention relates to PRO proteins and coding sequences. The  
 CC present sequence is one such PRO protein. It was found that the PRO genes  
 CC are amplified in the genome of tumour cells. The gene amplification is  
 CC expected to be associated with the overexpression of the gene product and  
 CC contributes to tumorigenesis. Therefore, antagonists of PRO proteins are  
 CC useful for the treatment of benign or malignant tumours, leukaemias,  
 CC lymphoid malignancies and other disorders such as neuronal, glial,  
 CC astrocytic, hypothalamic, glandular, epithelial, inflammatory and  
 CC immunologic disorders.  
 XX SQ Sequence 366 AA:  
 Query Match 77.0%; Score 67; DB 22; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGALVPRRLQ 13  
 Db 353 casdgalvprrlq 365  
 XX DE Human PRO317 protein.  
 XX AC AAB80231;  
 XX DT 24-APR-2001 (first entry)  
 XX OS Homo sapiens.  
 XX PN WO200104311-A1.  
 XX PD 18-JAN-2001.  
 XX PF 22-FEB-2000; 2000WO-US04414.  
 XX PR 07-JUL-1999; 99US-0143049.  
 XX PR 26-JUL-1999; 99US-0145698.  
 XX PR 28-JUL-1999; 99US-0146222.  
 XX PR 13-SEP-1999; 99WO-US20944.

RESULT 14  
 AAB80231  
 ID AAB80231 standard; Protein; 366 AA.  
 XX AC AAB80231;  
 XX DT 24-APR-2001 (first entry)  
 XX DE Human PRO317 protein.  
 XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 antiparkinsonian nootropic; neuroprotective; pulmonary; cardiant;  
 antiangiogenic; vasoactive; antisthmatic; antirheumatic; cancer;  
 antiarrhythmic; antiinertility; antidiabetic; antiviral; diabetes;  
 ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 ischaemia; inflammation.  
 XX OS Homo sapiens.  
 XX PN WO200104311-A1.  
 XX PD 18-JAN-2001.  
 XX PF 22-FEB-2000; 2000WO-US04414.  
 XX PR 07-JUL-1999; 99US-0143049.  
 XX PR 26-JUL-1999; 99US-0145698.  
 XX PR 28-JUL-1999; 99US-0146222.  
 XX PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US1547.  
 PR 05-OCT-1999; 99WO-US2089.  
 PR 29-NOV-1999; 99WO-US20914.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 16-DEC-1999; 99WO-US0095.  
 PR 20-DEC-1999; 99WO-US0911.  
 PR 20-DEC-1999; 99WO-US0999.  
 PR 05-JAN-2000; 99WO-US0219.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Ashkenazi AJ, Botstein D, Desnoyers L, Baton DL, Ferrara N, Ferrara N;  
 PR Fivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Goowski PJ, Grimaldi CJ, Gurney AL, Hillian KJ, Hlajavik IJ;  
 PI Mother JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 DR WPI: 2001-081051/09.  
 DR N-PSDB; AAF7392.  
 XX PT Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease) -  
 XX CC Claim 1; Fig 42; 393pp; English.  
 XX CC The present sequence is one of sixty one novel secreted and  
 CC transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding angiogenesis, ischaemias such as coronary  
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,  
 CC rheumatoid arthritis, multiple sclerosis) infertility, AIDS and  
 CC diabetes and retinal disorders such as retinitis pigmentosum.  
 CC The PRO nucleic acids have applications in molecular biology, including  
 CC use as hybridization probes, and in chromosome and gene mapping.  
 XX SQ Sequence 366 AA;

Query Match 77.0%; Score 67; DB 22; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 0.00078;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASDGALVPRRLQ 13  
 Db 353 casdgalvprrlq 365

RESULT 15  
 AAB19837  
 ID AAB19837 standard; Protein; 366 AA.  
 XX AC AAB19837;  
 XX DT 05-MAR-2001 (first entry)  
 XX DE Endometrial bleeding associated factor (ebaf) protein.  
 XX KW Endometrial bleeding associated factor; ebaf; human;  
 KW chromosome 1q2.1; neurodegenerative disease; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's chorea; dementia;  
 KW amytrophic lateral sclerosis; Pick's disease; therapy.  
 XX OS Homo sapiens.  
 XX PN WO200066068-A2.  
 XX PD 09-NOV-2000.

XX  
PF 28-APR-2000; 2000WO-US11623.  
XX  
PR 29-APR-1999; 99US-030204.  
XX  
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
XX  
PI Tabibzadeh S;  
XX  
DR WPI; 2001-040876/05.  
DR N-PSDp; AAA88913.  
XX  
PR Inducing growth and enhancing survival of nervous tissue by contacting  
PR with endometrial bleeding associated factor protein .  
XX  
: Disclosure; Fig 2; 23pp; English.

XX  
CC The present sequence is that of human endometrial bleeding  
CC associated factor (ehaf). A claimed method for inducing growth  
CC and enhancing survival of nervous tissue comprises contacting the  
CC tissue with ehaf or a nucleic acid encoding ehaf in vitro or in  
CC vivo. The method can be used to treat damaged or degenerated  
CC nervous tissue resulting from injury associated with trauma,  
CC diabetes, kidney dysfunction, ischaemia or use of therapeutic  
CC agents, or to treat a neurodegenerative disease such as Alzheimer's  
CC disease, Parkinson's disease, Huntington's chorea, amyotrophic  
CC lateral sclerosis, dementia, or Pick's disease (all claimed).  
XX  
SO Sequence 366 AA;

	Query Match	Match	Score	Length
	Best	Local Similarity	67;	2278;
	Matches	100.0%;	Pred. No.	366;
	13;	Conservative	0.00078;	
		0;	Mismatches	
			Indels	
			0;	Gaps

Qy 1 CASDGALVPRLQ 13  
Db 353 casdgalvprlq 365

Search completed: September 10, 2002, 10:45:12  
Job time: 265 sec

GenCore version 4.5  
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2002, 10:44:22 ; Search time 25.08 Seconds  
 (without alignments)  
 110,364 Million cell updates/sec

Title: US-09-674-254-3  
 Perfect score: 87  
 Sequence: 1 CASDGALVPRRLQHQP 16

Scoring table: BLOSUM62  
 Gapopen 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
 Maximum Match 1008  
 Listing first 45 summaries

Database : SPTRMBL19;\*

- 1: sp\_archaea;\*
- 2: sp\_bacteria;\*
- 3: sp\_fungi;\*
- 4: sp\_human;\*
- 5: sp\_invertebrate;\*
- 6: sp\_mammal;\*
- 7: sp\_mhc;\*
- 8: sp\_organelle;\*
- 9: sp\_phage;\*
- 10: sp\_plant;\*
- 11: sp\_rabbit;\*
- 12: sp\_virus;\*
- 13: sp\_vertebrate;\*
- 14: sp\_unclassified;\*
- 15: sp\_virus;\*
- 16: sp\_bacteria;\*
- 17: sp\_archaea;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	44	50.6	67	Q9UHN8	Q9uhn8 homo sapien
2	44	50.6	99	Q9UT41	Q9ui41 homo sapien
3	44	50.6	120	Q9UHM7	Q9uhm7 homo sapien
4	44	50.6	152	Q9UBR5	Q9ubr5 homo sapien
5	44	50.6	219	12 071131	071131 prunus necr
6	44	50.6	224	12 Q9YKE6	Q9yke6 prunus necr
7	44	50.6	224	12 Q9YKE3	Q9yke3 prunus necr
8	44	50.6	224	12 070915	070915 prunus necr
9	44	50.6	224	12 070917	070917 prunus necr
10	44	50.6	224	12 Q9IMR7	Q9imr7 prunus necr
11	44	50.6	224	12 09IMR5	09imr5 prunus necr
12	44	50.6	224	12 Q9IMR2	Q9imr2 prunus necr
13	44	50.6	224	12 Q9IMQ9	Q9imq9 prunus necr
14	44	50.6	224	12 Q9IMQ7	Q9imq7 prunus necr
15	44	50.6	224	12 Q9IMQ3	Q9imq3 prunus necr
16	44	50.6	224	12 Q9IMQ1	Q9imq1 prunus necr

## ALIGNMENTS

RESULT 1  
 Q9UHN8 ID Q9UHN8  
 AC Q9UHN8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DP 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CHEMOKINE-LIKE FACTOR 3.  
 GN CKLF3.  
 OS Homo sapiens (Human),  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Han W.L.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF135381; AAF198001;  
 SQ SEQUENCE 67 AA; 7652 MN; 7BBB754D8880F1F9 CRC64;

Query Match Score 44; DB 4; Length 67;  
 Best Local Similarity 50.6%; Pred. No. 2.1;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CASDGALVPRRLQHRP 16  
 | : ||| : | : |  
 Db 36 CLADGALIYRKLLFNP 51

RESULT 2  
 Q9UI41 ID Q9UI41  
 AC Q9UI41;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DP 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CHEMOKINE-LIKE FACTOR 1.  
 GN CKLF1.

OS Homo sapiens (Human); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo .	RC TISSUE-PANCREAS;
NCBI_TAXID=9606;	RA Zhang J.-S.; Nelson M.; Wang L.; Smith D.I.; Smith D.I.;
RN [1]	RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.	RN [2]
RX MEDLINE=21308461; PubMed=11415443;	RP SEQUENCE FROM N.A.
RA Han W.; Lou Y.; Tang J.; Zhang Y.; Chen Y.; Li Y.; Gu W.; Huang J.; Gui L.; Tang Y.; Li F.; Song Q.; Di C.; Wang L.; Shi Q.; Sun R., XIA D.; Rui M.; Tang J.; Ma D.;	RA Han W.; Gu W.; Li Y.; Zhang Y.; Song Q.; Di C.; Ma D.;
RA "Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity.";	RA Han W.; Gu W.; Li Y.; Zhang Y.; Zhou J.; Shen Y.; Wu X.Y.; Guan Z.Q.; Wang L.; Fan H.Y.; Mao Y.F.; Dai M.; Huang Q.H.; Chen S.J.; Chen Z.;
RT Biochem. J. 357:127-135 (2001).	RT "Human full length cDNA cloned from cd34+ stem cells.";
DR EMBL: AFO06895; AAF06722; 1;	RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 99 AA; 10923 MW; 1F5EBR5AA7A9479E CRC64;	RN [4]
RC TISSUE-PANCREATIC ADENOCARCINOMA;	RP SEQUENCE FROM N.A.
RA Strausberg R.;	RC TISSUE-PANCREATIC ADENOCARCINOMA;
RN [5]	RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	RN [6]
DR AF057306; AAF21255; 1;	DR AF057306; AAF21255; 1;
DR AF135380; AAF19519; 1;	DR AF135380; AAF19519; 1;
DR AF151058; AAF36144; 1;	DR AF151058; AAF36144; 1;
DR BC004380; AAH04380; 1;	DR BC004380; AAH04380; 1;
KW Transmembrane.	KW Transmembrane.
SQ SEQUENCE 152 AA; 17170 MW; 6149D62B6AEFD9F3 CRC64;	RN [7]
Query Match Score 44; DB 4; Length 99;	Query Match Score 44; DB 4; Length 152;
Best Local Similarity 50.6%; Pred. No. 3.1;	Best Local Similarity 50.6%; Pred. No. 4.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CASDGALVPRRLQHRP 16	Qy 1 CASDGALVPRRLQHRP 16
:      :   :	:      :   :
Db 68 CLADGALIYRKLLFNP 83	Db 121 CLADGALIYRKLLFNP 136
RESULT 3	RESULT 5
Q9UHM7 ID O71131 PRELIMINARY; PRT; 120 AA.	Q9UHM7 ID O71131 PRELIMINARY; PRT; 219 AA.
AC Q9UHM7; ID O71131 PRELIMINARY; PRT; 219 AA.	AC Q9UHM7; ID O71131 PRELIMINARY; PRT; 219 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHEMOKINE-LIKE FACTOR 4.	DE CORT PROTEIN (FRAGMENT)
GN CKLF4.	GN PRUNUS NECROTIC RINGSPOOT VIRUS.
OS Homo sapiens (Human).	OS PRUNUS NECROTIC RINGSPOOT VIRUS.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo .	OC PRUNUS NECROTIC RINGSPOOT VIRUS.
NCBI_TAXID=9606;	OC SSRNA positive-strand viruses, no DNA stage. Bromoviridae;
RN [1]	OC IILARVIRUS.
RP SEQUENCE FROM N.A.	OX NCBI_TAXID=37733;
RA Han W.L.;	RN [1]
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	RP SEQUENCE FROM N.A.
DR EMBL: AF145216; AAF19350; 1;	RC SPRAIN-CH61;
SQ SEQUENCE 120 AA; 13899 MW; BF0C011077F24C13 CRC64;	RX MEDLINE=98343741; PubMed=96800147;
Query Match Score 44; DB 4; Length 120;	RA Hammond R.W.; Crosslin J.M.;
Best Local Similarity 50.0%; Pred. No. 3.7;	RT "Virulence and molecular polymorphism of Prunus necrotic ringspot virus isolates."
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	RT J. Gen. Virol. 79:1815-1823(1998).
Qy 1 CASDGALVPRRLQHRP 16	RL DR AF034989; AAC41025; 1;
:      :   :	DR InterPro; IPR002881; IILAR-coat.
Db 89 CLADGALIYRKLLFNP 104	DR PFM; PF01767; IILAR-coat; 1.
RESULT 4	Query Match Score 44; DB 12; Length 219;
Q9UBRS ID P01767 PRELIMINARY; PRT; 152 AA.	Best Local Similarity 60.0%; Pred. No. 6.3;
AC Q9UBRS; ID P01767 PRELIMINARY; PRT; 152 AA.	Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)	Qy 1 CASDGALVPRRLQHR 15
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Db 20 CRPNGLVPLRQQQR 34
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	RN [1]
DE MGC:101658.	RP SEQUENCE FROM N.A.
GN C32 OR CKLF2.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo .
OS NCBI_TAXID=9606;	OC NCBI_TAXID=9606;
RN [1]	RP SEQUENCE FROM N.A.

Q9YKE6	PRELIMINARY;	PRT;	224 AA.		DR EMBL; AJ133208; CAB37310.1; -.
Q9YKE5;					DR EMBL; AF170160; AAB89709.1; -.
AC					DR InterPro; IPR02681; Ilar_coat.
DT	01-MAY-1999 (TREMBLrel. 10, Created)				DR Pfam; PF01787; Ilar_coat; 1.
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)				KW Coat protein.
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				SQ SEQUENCE 224 AA; 24927 MW;
DE	COAT PROTEIN (CAPSID PROTEIN).				E215BCEED1C0703F CRC64;
GN	CP.				
OS	Prunus necrotic ringspot virus.				
OC	Virus; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;				
OC	Ilarvirus.				
OX	NCBI_TAXID=37733;				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=NCPCHIT.MAV1;				
RA	Aparicio F., Mytta A., Di Terlizzi B., Pallas V.;				
RT	"Molecular variability among fifteen isolates of Prunus necrotic				
RR	ringspot virus (PNSRV) from six different Prunus species.";				
RR	Submitted (FEB-1999) to the EMBL/GenBank/DBJ/NCBI databases.				
[2]					
RN	SEQUENCE FROM N.A.				
RP	STRAIN=N4/B, AND UN;				
RX	MEDLINE=20349238; PubMed=10893149;				
RA	Vaskova D., Petzlik K., Karesova R.;				
RT	"Variability and molecular typing of the woody-tree infecting prunus				
RT	necrotic ringspot ilarvirus.";				
RL	Arch. Virol. 145:699-709(2000).				
DR	EMBL; AJ13205; CAB37307.1; -.				
DR	EMBL; AF170165; AAF89719.1; -.				
DR	EMBL; AF170163; AAF89715.1; -.				
DR	InterPro; IPR003681; Ilar_coat.				
DR	Pfam; PF01787; Ilar_coat; 1.				
KW	Coat_protein.				
SQ	SEQUENCE 224 AA; 24911 MW; DE0079AED4E475D CRC64;				
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
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Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Db	[1] :				
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Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
20 CHPNGALVPLRAQQR 34					
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
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Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
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Db	[1] :				
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
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Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0%; Pred. No. 7;				
Matches	9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;				
OY	1 CASDGALVPRRLQHR 15				
Db	[1] :				
20 CHPNGALVPLRAQQR 34					
Query Match	50.6%; Score 44; DB 12; Length 224;				
Best Local Similarity	60.0				

RL Eur. J. Plant Pathol. 104:155-161(1998).  
DR EMBL; AF013286; AAC16501.  
DR InterPro; IPR002681; Ilar\_coat.  
DR Pfam; PF01787; Ilar\_coat\_1.  
SQ SEQUENCE 224 AA; 24939 MW; 8D03DAAEDC21BACF CRC64;

Query Match 50.6%; Score 44; DB 12; Length 224;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 CASDGALYPRRQLQR 15  
| :|||||| | | |  
Db 20 CYPNGALVPLRAQQR 34

RESULT 10  
Q9IMR7 PRELIMINARY; PRT; 224 AA.  
ID Q9IMR7; PRELIMINARY; PRT; 224 AA.  
AC Q9IMR7; PRELIMINARY; PRT; 224 AA.  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE CAPSID PROTEIN.  
CP.  
Prunus necrotic ringspot virus.  
OS ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
OC Ilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PS 7/11;  
MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
necrotic ringspot ilarvirus";  
RT necrotic ringspot ilarvirus."  
RL Arch. Virol. 145:699-709(2000).  
DR EMBL; AF170161; AAF699709.  
DR InterPro; IPR002681; Ilar\_coat.  
DR Pfam; PF01787; Ilar\_coat\_1.  
SQ SEQUENCE 224 AA; 24965 MW; 9D1EB6CBC04DDFDA CRC64;

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DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
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Prunus necrotic ringspot virus.  
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OC Ilarvirus.  
OX NCBI\_TaxID=37733;  
RN [1]  
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RC STRAIN=PS 7/12;  
MEDLINE=20349238; PubMed=10893149;  
RA Vaskova D., Petrzik K., Karesova R.;  
RT "Variability and molecular typing of the woody-tree infecting prunus  
necrotic ringspot ilarvirus";  
RL Arch. Virol. 145:699-709(2000).

RL Arch. Virol. 145:699-709 (2000).  
 DR EMBL; AF170166; AAF89721.1;  
 DR InterPro; IPR003345; CytC\_heme\_bind.  
 DR InterPro; IPR003681; Ilar\_coat.  
 DR Pfam; PF01787; Ilar\_coat; 1.  
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 RA Vaskova D.; Petrik K.; Karesova R.;  
 RT "Variability and molecular typing of the woody-tree infecting prunus  
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 RT Arch. Virol. 145:699-709 (2000).  
 DR EMBL; AF170167; AAF89723.1;  
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 DR Pfam; PF01787; Ilar\_coat; 1.  
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 RC STRAIN=NA\_HRB; MEDLINE=20349238; PubMed=10893149;

RA Vaskova D.; Petrik K.; Karesova R.;  
 RT "Variability and molecular typing of the woody-tree infecting prunus  
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 RT Arch. Virol. 145:699-709 (2000).  
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 DR InterPro; IPR000345; CytC\_heme\_bind.  
 DR InterPro; IPR002681; Ilar\_coat.  
 DR Pfam; PF01787; Ilar\_coat; 1.  
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Qy 1 CASDGALVPLRAQQR 34  
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